

OM protein - protein search, using sw model

Run on: April 23, 2004, 14:55:02 ; Search time 72 Seconds
(without alignments)
6533.911 Million cell updates/sec

Title: US-10-697-263-2
Perfect score: 8740
Sequence: 1 MGCCRLGCGCSVAHSVSG.....RNREKRRALLYKHNIAQVR 1665

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: Geneseqp29Jan04:*
2: Geneseqp1980s:*
3: Geneseqp1980s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8740	100.0	1665	5	AAO15372 Human myo
2	8727	99.9	1665	5	AAE24151 Human kin
3	8423	96.4	2630	6	ABG76186 Human ser
4	8423	96.4	2630	6	ABG76187 Human ser
5	8417	96.3	2596	4	AA330569 A splice
6	8403	96.1	1618	4	AA330569 Human pro
7	8399	96.1	1610	4	AA330568 A full le
8	7069	80.9	1351	4	AA330567 Amino aci
9	4533	51.9	871	5	AAE16274 Human kin
10	4529	51.8	871	4	AA330570 A splice
11	2447.5	28.0	548	4	AA330571 A full le
12	2415.5	27.6	548	4	AA330572 A full le
13	1973	22.6	2286	4	AA330573 Novel pro
14	1973	22.6	2380	5	AA330574 Human kin
15	1973	22.6	3208	7	AA330575 Human KPP
16	1973	22.6	3267	7	AA330576 Human NOV
17	1967.5	22.5	3268	7	AA330577 Human kin
18	1931	22.1	3252	7	AA330578 Human NOV
19	1913	21.9	2231	7	AA330579 Human KIA
20	1864	21.3	3262	7	AA330580 Mouse ser
21	1746.5	20.0	3186	7	AA330581 Human NOV
22	632.5	7.2	282	7	AA330582 Human NOV
23	607	6.9	127	5	AA330583 Human kin
24	592.5	6.8	2861	2	AAW27227 Human TRI
25	592.5	6.8	2861	4	ABG17024 Novel hum

26	592.5	6.8	2861	4	AAG68192	GTPase pr
27	592.5	6.8	2861	6	ABR41116	Human GTP
28	592.5	6.8	2861	6	ABU70968	Human adi
29	592.5	6.8	2861	7	ADB98736	Human GTP
30	592.5	6.8	2861	7	ADB98736	Human GTP
31	592.5	6.8	2861	7	ADB98736	Human GTP
32	592.5	6.8	2861	7	ADB98736	Human GTP
33	592.5	6.8	2861	7	ADB98736	Human GTP
34	592.5	6.8	2861	7	ADB98736	Human GTP
35	592.5	6.8	2861	7	ADB98736	Human GTP
36	592.5	6.8	2861	7	ADB98736	Human GTP
37	592.5	6.8	2861	7	ADB98736	Human GTP
38	592.5	6.8	2861	7	ADB98736	Human GTP
39	592.5	6.8	2861	7	ADB98736	Human GTP
40	592.5	6.8	2861	7	ADB98736	Human GTP
41	592.5	6.8	2861	7	ADB98736	Human GTP
42	592.5	6.8	2861	7	ADB98736	Human GTP
43	592.5	6.8	2861	7	ADB98736	Human GTP
44	592.5	6.8	2861	7	ADB98736	Human GTP
45	592.5	6.8	2861	7	ADB98736	Human GTP

ALIGNMENTS

RESULT 1	
AAO15372	
ID	AAO15372 standard; protein; 1665 AA.
XX	AAO15372;
AC	AAO15372;
XX	19-SEP-2002 (first entry)
DT	19-SEP-2002 (first entry)
XX	Human myosin light chain kinase subfamily-related kinase protein.
DE	Human; gene therapy; chromosome 1; kinase protein;
KW	myosin light chain kinase subfamily; kinase protein-mediated disease;
KW	transgenic animal.
XX	Homo sapiens.
OS	WO2002040683-A2.
XX	23-MAY-2002.
PD	22-OCT-2001; 2001WO-US032616.
PF	14-NOV-2000; 2000US-00711134.
XX	17-MAY-2001; 2001US-00858664.
PR	(PEKE) PE CORP NY.
XX	Wei M, Ketchum K, Di Francesco V, Beasley EM;
PI	WFI; 2002-500223/53.
XX	N-PSDB; AAL43908, AAL43909.
DR	New kinase proteins related to myosin light chain kinase subfamily and
XX	encoding polynucleotide, useful for diagnosing, treating disease or
PT	condition mediated by the kinase protein and for identifying modulators.
XX	Claim 1; Fig 2; 96pp; English.
XX	The invention comprises the amino acid and coding sequences (located on
CC	chromosome 1) of a human kinase protein that is related to the myosin
CC	light chain kinase subfamily. The human kinase DNA and protein sequences
CC	of the invention are useful for identifying agents that modulate the
CC	activity of the human kinase protein. Kinase-modulating agents are useful
CC	for treating a disease or condition mediated by a human kinase protein.
CC	The human kinase DNA sequences can be used to produce transgenic animals
CC	which are useful for studying the function of kinase proteins and
CC	identifying/evaluating modulators of kinase protein activity. The present
CC	amino acid sequence represents the human kinase protein of the invention

XX SQ Sequence 1665 AA;

Query Match 100.0%; Score 8740; DB 5; Length 1665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGCCRLGGCGGSAVHSVSGGLTNHP	SMVCGWHFGL	CGWGGHSSLPALPGPSPMQVTI	60
DB	1	MGCCRLGGCGGSAVHSVSGGLTNHP	SMVCGWHFGL	CGWGGHSSLPALPGPSPMQVTI	60
QY	61	EDVQATGCTAQAFAEII	EGDPQPSVTYKDSVOLVDSTRL	SOQOEGTYSVLVRHVASKD	120
DB	61	EDVQATGCTAQAFAEII	EGDPQPSVTYKDSVOLVDSTRL	SOQOEGTYSVLVRHVASKD	120
QY	121	AGVYTCLAQNGGQVLCVHAEII	LVGGDNEPSEKSHRRKLHSPYEVKEE	IGRGVGFVK	180
DB	121	AGVYTCLAQNGGQVLCVHAEII	LVGGDNEPSEKSHRRKLHSPYEVKEE	IGRGVGFVK	180
QY	181	RVQHGKNTLCAAKFIP	LSRTRAQVREIRDI	LAALSHPLVTGLDQFETRKTLIIILEL	240
DB	181	RVQHGKNTLCAAKFIP	LSRTRAQVREIRDI	LAALSHPLVTGLDQFETRKTLIIILEL	240
QY	241	CSSEELLRLRYKGVVTEAEVKYI	QQLVEGLHYLHSHGVHLHDIKPSNLMVHPAREDI		300
DB	241	CSSEELLRLRYKGVVTEAEVKYI	QQLVEGLHYLHSHGVHLHDIKPSNLMVHPAREDI		300
QY	301	KICDFGFAQNTIPAELOFSOYSGSPFV	PEIIQONPVSEASDIWAMGVI	SYLSLTGSSPF	360
DB	301	KICDFGFAQNTIPAELOFSOYSGSPFV	PEIIQONPVSEASDIWAMGVI	SYLSLTGSSPF	360
QY	361	AGESDRATLLNVLEGRVSNWSPMAH	ISEDADKFIKATLQRAQAPRPSAAQCLSHPWFLK		420
DB	361	AGESDRATLLNVLEGRVSNWSPMAH	ISEDADKFIKATLQRAQAPRPSAAQCLSHPWFLK		420
QY	421	SMPAEAEHPIFINTKQLKFL	LARSQRWSILMSYKSLVNRISPEILLRPPDPS	LGVARHLC	480
DB	421	SMPAEAEHPIFINTKQLKFL	LARSQRWSILMSYKSLVNRISPEILLRPPDPS	LGVARHLC	480
QY	481	RTGCGSSSSSSNDNELAPPA	RAKSLPPSPVTHSPLHPRGFLRPSASLPEAEASERST		540
DB	481	RTGCGSSSSSSNDNELAPPA	RAKSLPPSPVTHSPLHPRGFLRPSASLPEAEASERST		540
QY	541	EAPAPPASPEGAGPPAAGCVP	PHSVIRSLFYHQAGSEPHGALAPGSRHPARRHLLK		600
DB	541	EAPAPPASPEGAGPPAAGCVP	PHSVIRSLFYHQAGSEPHGALAPGSRHPARRHLLK		600
QY	601	GGYIAGALPGLREPLMEHRVLEBAARE	EQATLLAKAPSFETALRLPASGTHLAPGSHS		660
DB	601	GGYIAGALPGLREPLMEHRVLEBAARE	EQATLLAKAPSFETALRLPASGTHLAPGSHS		660
QY	661	LEHDSPTSPSSSEACGAQRLP	APSGGAPIRDMGHPQSKQLPSTGGHPGTAQPERPS		720
DB	661	LEHDSPTSPSSSEACGAQRLP	APSGGAPIRDMGHPQSKQLPSTGGHPGTAQPERPS		720
QY	721	PDSNMGQAPAPCHPKGSAPOEGCS	PHPAVAPCPGSPFGSCKEAPLVPSSPFLQPOA		780
DB	721	PDSNMGQAPAPCHPKGSAPOEGCS	PHPAVAPCPGSPFGSCKEAPLVPSSPFLQPOA		780
QY	781	PPAPAKASPLDLSKMGPGDISL	PGRPKPGPCSSPGSASQASSQVSSLRVSSQVGTETPG		840
DB	781	PPAPAKASPLDLSKMGPGDISL	PGRPKPGPCSSPGSASQASSQVSSLRVSSQVGTETPG		840
QY	841	PSLDAEGWTQAEADLSDSTPTL	QRPQEQVTMRKPSLGGRGYAGVAGTGF	FAFGDAGCM	900
DB	841	PSLDAEGWTQAEADLSDSTPTL	QRPQEQVTMRKPSLGGRGYAGVAGTGF	FAFGDAGCM	900
QY	901	LGQCPMWARIAWVSQSEEEQE	AREAESEEQEARESPLOVSARPEVPEVGRAPTR		960
DB	901	LGQCPMWARIAWVSQSEEEQE	AREAESEEQEARESPLOVSARPEVPEVGRAPTR		960
QY	961	SSPEPTPHEDIGQVSLVQIR	LDSCGDAEADTISLDISEVDPAYLNLSLDYIKYLPFEEM		1020

DB	961	SSPEPTPHEDIGQVSLVQ	IRLDSCAAADTISLDISEVDPAYLNLSLDYIKYLPFEEM	1020
QY	1021	IFRKVPKSAQPEPPSPMAE	BELEAFEPPTWPGELPGHAGLEITBESDNDALLAEAAV	1080
DB	1021	IFRKVPKSAQPEPPSPMAE	BELEAFEPPTWPGELPGHAGLEITBESDNDALLAEAAV	1080
QY	1081	GRKKNWSPRSRUPHPPGR	HLPLDEPAELGLRVRVXASVEHSRIILKGRPEGLEKGGPR	1140
DB	1081	GRKKNWSPRSRUPHPPGR	HLPLDEPAELGLRVRVXASVEHSRIILKGRPEGLEKGGPR	1140
QY	1141	KKPGCLASFRLSGLSKW	DRAPTFRELSDETVVLGQSVTLACQVSAQAPAAQATWSKDAPL	1200
DB	1141	KKPGCLASFRLSGLSKW	DRAPTFRELSDETVVLGQSVTLACQVSAQAPAAQATWSKDAPL	1200
QY	1201	ESSSRVLIATLKNPQLT	ILVVVAEDLVYTCVSNALGTVTTTGVLRKARPPSSPCP	1260
DB	1201	ESSSRVLIATLKNPQLT	ILVVVAEDLVYTCVSNALGTVTTTGVLRKARPPSSPCP	1260
QY	1261	DIGEVYADGVLLVWKPV	ESYGPVTYIQCSEGGSWTTLASDIFDCCYLTSLSRGGTYT	1320
DB	1261	DIGEVYADGVLLVWKPV	ESYGPVTYIQCSEGGSWTTLASDIFDCCYLTSLSRGGTYT	1320
QY	1321	FRTACVSKAGKGPYSSP	SEQVLLGGFSLHASEEESQGRSAQLPSTKTAFQTQGRGF	1380
DB	1321	FRTACVSKAGKGPYSSP	SEQVLLGGFSLHASEEESQGRSAQLPSTKTAFQTQGRGF	1380
QY	1381	SVVRQCWEKASGRALA	AKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAVLSPRHLVL	1440
DB	1381	SVVRQCWEKASGRALA	AKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAVLSPRHLVL	1440
QY	1441	ILELCSGPELLPCLAE	RASYSSEVKDYLMQMLSATQYLHNOHILHLDURSENMITEYN	1500
DB	1441	ILELCSGPELLPCLAE	RASYSSEVKDYLMQMLSATQYLHNOHILHLDURSENMITEYN	1500
QY	1501	LLKVVYDLGNAQSL	SOEKVLPDSFKDYLETMAPELLEGQGVPTDIAIGVTAFTMLSA	1560
DB	1501	LLKVVYDLGNAQSL	SOEKVLPDSFKDYLETMAPELLEGQGVPTDIAIGVTAFTMLSA	1560
QY	1561	EYPVSSGADLQGLKGL	VLRSVCVAGLSCGAVAFRLSTLCAQWPGRPCASSCLOCPW	1620
DB	1561	EYPVSSGADLQGLKGL	VLRSVCVAGLSCGAVAFRLSTLCAQWPGRPCASSCLOCPW	1620
QY	1621	LTEGPGACSPAPVPT	PTAFRLRVFVRNREKRALLYKRHNLAQVR	1665
DB	1621	LTEGPGACSPAPVPT	PTAFRLRVFVRNREKRALLYKRHNLAQVR	1665
XX	AAE24151	standard; protein; 1665 AA.		
XX	AAE24151;			
DT	23-SEP-2002	(first entry)		
XX	Human kinase (PKIN)-22	protein.		
DE	Human; kinase; PKIN; cancer; immune system disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolemia; obesity; gene therapy; cytostatic; anti-HIV; neuroprotective; hepatotropic; hypotensive; cardiac; nephrotropic; hyperlipidaemia; enzyme.			
XX	Homo sapiens.			
XX	Key	Location/Qualifiers		
PH	Key	68..128		
FT	Domain	/note= "Immunoglobulin domain"		
FT	Domain	165..418		

RESULT 2

AAE24151

ID AAE24151 standard; protein; 1665 AA.

XX AAE24151;

DT 23-SEP-2002 (first entry)

XX Human kinase (PKIN)-22 protein.

Human; kinase; PKIN; cancer; immune system disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolemia; obesity; gene therapy; cytostatic; anti-HIV; neuroprotective; hepatotropic; hypotensive; cardiac; nephrotropic; hyperlipidaemia; enzyme.

XX Homo sapiens.

XX Key

PH Key

FT Domain

FT Domain

FT Domain

FT Domain /note= "Eukaryotic protein kinase domain"
 FT 167..401
 FT /note= "Protein kinase domain"
 FT 1174..1235
 FT /note= "Immunoglobulin domain"
 FT 1369..1621
 FT /note= "Eukaryotic protein kinase domain"
 FT 1372..1606
 FT /note= "Protein kinase domain"
 XX
 XX WO200233099-A2.
 XX
 XX 25-APR-2002.
 XX
 XX 20-OCT-2001; 2001WO-US047728.
 XX
 XX 20-OCT-2000; 2000US-0242410P.
 XX
 XX 27-OCT-2000; 2000US-0244068P.
 XX
 XX 03-NOV-2000; 2000US-0245708P.
 XX
 XX 09-NOV-2000; 2000US-0247672P.
 XX
 XX 16-NOV-2000; 2000US-0249565P.
 XX
 XX 22-NOV-2000; 2000US-0252730P.
 XX
 XX 01-DEC-2000; 2000US-0250807P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Gururajan R, Baughn MR, Wadia NK, Elliott VS, Xu Y, Arvizu C;
 PI Yao MG, Ramkumar J, Ding L, Tang Y, Hafalia AdA, Nguyen DB;
 PI Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;
 PI Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;
 PI Thangavelu K, Khan FA, Ison CH;
 XX
 XX WPI: 2002-454603/48.
 XX
 XX N-PSDB; AAD38865.
 XX
 XX New human kinase polypeptide, for diagnosing, preventing and treating
 PT cancer, immune system disorders, growth and development disorders,
 PT cardiovascular disorders and lipid disorders.
 XX
 XX Claim 1: Page 182-186; 210pp; English.
 XX
 XX The invention relates human kinases (PKIN) and their corresponding
 CC nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
 CC treating and preventing cancer, an immune system disorder (e.g., acquired
 CC immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,
 CC atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
 CC growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
 CC cardiovascular disorder (e.g., hypertension, myocardial infarction,
 CC Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
 CC Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,
 CC hyperlipidemia, obesity), and for assessing the effects of exogenous
 CC compounds. Anti-PKIN antibody is useful in a diagnostic test for a
 CC condition or a disease associated with the expression of PKIN in a
 CC biological sample. A composition comprising PKIN or an agonist or
 CC antagonist of PKIN is useful for treating a disease or condition
 CC associated with decreased or increased expression of functional PKIN.
 CC PKIN is useful in a number of drug screening techniques and to analyse
 CC the proteome of a tissue or cell type. PKIN DNA is useful for creating
 CC knockin humanised animals or transgenic animals to model human diseases,
 CC and in somatic or germline gene therapy. The present sequence is human
 CC PKIN protein
 XX
 XX Sequence 1665 AA;
 XX
 XX Query Match 99.9%; Score 8727; DB 5; Length 1665;
 XX Best Local Similarity 99.9%; Pred No 0;
 XX Matches 1663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGCCRLGCGGCSVAHVSQGLTNHPSVMVCGWHFGLCGWGGGLHSSLPALPGPPSMQVTI 60
 DB 1 MGCCRLGCGGCSVAHVSQGLTNHPSVMVCGWHFGLCGWGGGLHSSLPALPGPPSMQVTI 60
 QY 61 EDVQAGTGTGTAQFAEIIIEGDPQPSVTWYKDSVQLVDSTRLSQQQEGTTSYLVLRHASKD 120

DB 61 EDVQAGTGTGTAQFAEIIIEGDPQPSVTWYKDSVQLVDSTRLSQQQEGTTSYLVLRHASKD 120
 QY 121 AGVYTCLAQNTGGVLCCKAEALLVLGDNEPDSEKSHRKLHSHFYEVKEIGRGVGFVK 180
 DB 121 AGVYTCLAQNTGGVLCCKAEALLVLGDNEPDSEKSHRKLHSHFYEVKEIGRGVGFVK 180
 QY 181 RVQHKGNKILCAAKFIPILRSRTRAQAYRERDILAAALSHPLVTGLLDQFETKTLILLEL 240
 DB 181 RVQHKGNKILCAAKFIPILRSRTRAQAYRERDILAAALSHPLVTGLLDQFETKTLILLEL 240
 QY 241 CSSELLDLRLYKGVVTEAEVKVYIQQVLEGLYHSHGVHLHDIKFSNIIIMVHPAREDI 300
 DB 241 CSSELLDLRLYKGVVTEAEVKVYIQQVLEGLYHSHGVHLHDIKFSNIIIMVHPAREDI 300
 QY 301 KICDFGFAQNTIPAELOPSQYSGSPFVSPEIQQNPVSEASDIWAMGVISYLSITCSPP 360
 DB 301 KICDFGFAQNTIPAELOPSQYSGSPFVSPEIQQNPVSEASDIWAMGVISYLSITCSPP 360
 QY 361 AGESDRATLLNVLGRVSWSPMAHLSADAKFIKATLQAPQAPSAACLSHPWFLK 420
 DB 361 AGESDRATLLNVLGRVSWSPMAHLSADAKFIKATLQAPQAPSAACLSHPWFLK 420
 QY 421 SMPAEAHFINTKQLKFLARSWORSIMSYKSTILVMSIPELLRGPPDSPSLGVARHLK 480
 DB 421 SMPAEAHFINTKQLKFLARSWORSIMSYKSTILVMSIPELLRGPPDSPSLGVARHLK 480
 QY 481 RTDGSSESSSSSSDNELAPPAPAKSLPSPVTHSPLHPRGFLRPPSASLPPEASERST 540
 DB 481 RTDGSSESSSSSSDNELAPPAPAKSLPSPVTHSPLHPRGFLRPPSASLPPEASERST 540
 QY 541 EAPAPPASPEGAGPPAAQGCVPFRHSVIRSLFYHOGSPSEHGALAPGSRHRPARRHLK 600
 DB 541 EAPAPPASPEGAGPPAAQGCVPFRHSVIRSLFYHOGSPSEHGALAPGSRHRPARRHLK 600
 QY 601 GYIAGALPGRLMEHRVLEEAAREQATLLAKAPSPETALRLPASGTHLAPGSHS 660
 DB 601 GYIAGALPGRLMEHRVLEEAAREQATLLAKAPSPETALRLPASGTHLAPGSHS 660
 QY 661 LEHDSPTSPRSSACGAEQRLPSAPGAPIRDMGHPOGSKQLPSTGGHGTACQRPSP 720
 DB 661 LEHDSPTSPRSSACGAEQRLPSAPGAPIRDMGHPOGSKQLPSTGGHGTACQRPSP 720
 QY 721 PDSPMGQAPFCHPKQSGAPQGGSPHPAPACPPGPPGSCKEAPLVSPSSPPLGQFQA 780
 DB 721 PDSPMGQAPFCHPKQSGAPQGGSPHPAPACPPGPPGSCKEAPLVSPSSPPLGQFQA 780
 QY 781 PPAPAKASPPLDKMGPGDLSLGRPKPGCSSPGSASQASSQVSSLRVSSQVGTPEG 840
 DB 781 PPAPAKASPPLDKMGPGDLSLGRPKPGCSSPGSASQASSQVSSLRVSSQVGTPEG 840
 QY 841 PSLDAEGWTQAEADLSSTPTLQRPQSVTWKPSLGGRGYAGVAGYGTAFGGDAGGM 900
 DB 841 PSLDAEGWTQAEADLSSTPTLQRPQSVTWKPSLGGRGYAGVAGYGTAFGGDAGGM 900
 QY 901 LQGGPMWARIWAVSQSEEEQEARAESQSEOEQEARAESPLPOVSARVPVVGRAPTR 960
 DB 901 LQGGPMWARIWAVSQSEEEQEARAESQSEOEQEARAESPLPOVSARVPVVGRAPTR 960
 QY 961 SSPEPTPWEDIGQVSLVQIRDLSDGABAADTISLIDISEVDPAYNLSDLDIKYLPPEFM 1020
 DB 961 SSPEPTPWEDIGQVSLVQIRDLSDGABAADTISLIDISEVDPAYNLSDLDIKYLPPEFM 1020
 QY 1021 IFRKVPKSAQPEPPSPMAEEELAEFPETWPCGLGPHAGLEITSESDVDALLAAAV 1080
 DB 1021 IFRKVPKSAQPEPPSPMAEEELAEFPETWPCGLGPHAGLEITSESDVDALLAAAV 1080
 QY 1081 GRKRWSSPSSLSLPHFPGRHPLDEPAELGLRERVKASVEHISRIILKGRPEGLEKGGPPR 1140
 DB 1081 GRKRWSSPSSLSLPHFPGRHPLDEPAELGLRERVKASVEHISRIILKGRPEGLEKGGPPR 1140
 QY 1141 KKPGLASFLSLGSLKSWDRAPTFLELSDETIVLQGSVTLACQVSAQAPAAQATWSKDGAPL 1200

Db 1141 KXPLASFLSGLKSWDRAPFTFLRELSDETIVVLGQSVTLACQVSAQPAQAQTSKDGAPL 1200
 QY 1201 ESSSRVLISATLKNFOLLTLVVAEDLGVVTCVSVALGTVTTTGVLRKAERPSSPCP 1260
 Db 1201 ESSSRVLISATLKNFOLLTLVVAEDLGVVTCVSVALGTVTTTGVLRKAERPSSPCP 1260
 QY 1261 DIGEVYADGVLLVWKPVSYGVTYIVQCSLEGGSWTTLASDIPDCCLYLSKLSRGTTYT 1320
 Db 1261 DIGEVYADGVLLVWKPVSYGVTYIVQCSLEGGSWTTLASDIPDCCLYLSKLSRGTTYT 1320
 QY 1321 FRTACVSKAGMGFYSPSEQVLLGQFSLASEEBSQGRSAQPLPSTTKTFAFQCIQGRF 1380
 Db 1321 FRTACVSKAGMGFYSPSEQVLLGQFSLASEEBSQGRSAQPLPSTTKTFAFQCIQGRF 1380
 QY 1381 SVVRCWEKASGRALAAKIIYPHKDKTAVLREYALKGLRHPLHAQHAAYLSRHLVL 1440
 Db 1381 SVVRCWEKASGRALAAKIIYPHKDKTAVLREYALKGLRHPLHAQHAAYLSRHLVL 1440
 QY 1441 LLELCGPELLPCLAEASYSSESEKQYLWQMLSATQYLHNQHLHLDLSENWITEYN 1500
 Db 1441 LLELCGPELLPCLAEASYSSESEKQYLWQMLSATQYLHNQHLHLDLSENWITEYN 1500
 QY 1501 LKVVLDLGNAGLSQEKVLPDKKDYLETWAPLEGGQAVPCTDIWAGTAFIMLSA 1560
 Db 1501 LKVVLDLGNAGLSQEKVLPDKKDYLETWAPLEGGQAVPCTDIWAGTAFIMLSA 1560
 QY 1561 EYPVSESGARDLQRLKGLVRLSRVAGLSGGAVAFRLSTLCAQWGRPCASSCLQCPW 1620
 Db 1561 EYPVSESGARDLQRLKGLVRLSRVAGLSGGAVAFRLSTLCAQWGRPCASSCLQCPW 1620
 QY 1621 LTEEGPACSRPAPVTFPTARLRVFRNREKERALLYKHNLAQVR 1665
 Db 1621 LTEEGPACSRPAPVTFPTARLRVFRNREKERALLYKHNLAQVR 1665

RESULT 3
 ABG76186
 ID ABG76186 standard; protein; 2630 AA.
 XX AC ABG76186;
 XX DT 09-MAY-2003 (first entry)
 XX DE Human serine/threonine or protein kinase 59079.
 XX Human; enzyme; serine/threonine kinase; protein kinase; 59079;
 KW cardiovascular disease; heart failure; myocardial infarction;
 KW blood vessel disorder; atherosclerosis; Kaposi's sarcoma; immunogen;
 KW blood platelet disorder; thrombocytopaenia; leukaemia; Hodgkin's disease;
 KW haemolytic anaemia; cellular proliferative disorder; cancer;
 KW protein kinase disorder; autoimmune disorder; diabetes mellitus;
 KW psoriasis; inflammatory bowel disease; rheumatoid arthritis;
 KW multiple sclerosis.
 XX OS Homo sapiens.
 XX PN US2002168742-A1.
 XX PD 14-NOV-2002.
 XX PF 15-FEB-2002; 2002US-00077130.
 XX PR 15-FEB-2001; 2001US-0269201P.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Kapeller-Libermann R, Acton SJ;
 XX WP1; 2003-298729/29.
 XX DR N-PSDB; ABX11641.
 XX PT Novel isolated human protein kinase, designated 59079 or 12599
 PT polypeptide, useful as diagnostic and therapeutic agents for preventing

PT cardiovascular diseases, proliferative disorders, and protein kinase
 PT disorders.
 XX Claim 8; Page 48-54; 119pp; English.
 CC The invention relates to an isolated human serine/threonine or protein
 CC kinase, 59079 or 12599 polypeptide, encoded by nucleic acid molecule
 CC comprising at least 85% identity to the nucleic acids appearing as
 CC ABX11641 and ABX11642 or their complement, a naturally occurring variant
 CC of the kinases or their fragments. Also included are a non-human host
 CC cell containing the nucleic acids, an antibody specific for the proteins,
 CC identifying a compound which binds to the kinase (by contacting the
 CC kinase or a cell expressing the kinase with a test compound and
 CC determining whether the kinase binds to the test compound), and modulating
 CC the activity of kinase using the identified compound. The kinases and
 CC their encoding nucleic acids are useful as diagnostic and therapeutic
 CC agents for preventing a disease or condition associated with an aberrant
 CC or unwanted 59079 or 12599 activity in a subject, including
 CC cardiovascular diseases such as heart failure, and myocardial infarction;
 CC disorders involving blood vessels such as atherosclerosis, and Kaposi's
 CC sarcoma; blood platelets disorder such as thrombocytopaenia, leukaemia;
 CC Hodgkin's disease, haemolytic anaemia; cellular proliferative disorders
 CC such as cancer; and protein kinase disorders such as autoimmune
 CC disorders, diabetes mellitus, psoriasis, inflammatory bowel disease,
 CC rheumatoid arthritis, and multiple sclerosis (many examples of diseases
 CC and disorders are included in the specification). The kinases, their
 CC encoding nucleic acids and antibodies are useful in screening assays,
 CC detection assays (e.g. forensic biology), and predictive medicine (e.g.
 CC pharmacogenomics). The kinases and their encoding nucleic acids are
 CC useful as query sequences to perform a search against public databases to
 CC identify other family members or related sequences. The present sequence
 CC represents kinase 59079
 XX SQ Sequence 2630 AA;

Query Match 96.4%; Score 8423; DB 6; Length 2630;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 53 PPSNQVTIEDVQAGTGTGTAQFAEIIIEGDPQSPVTVTKDSVQLVDSTRLSQQEGTYSIV 112
 Db 1018 PPSNQVTIEDVQAGTGTGTAQFAEIIIEGDPQSPVTVTKDSVQLVDSTRLSQQEGTYSIV 1077
 QY 113 LRHVASKDAGVYTCLAQNTGGQVLCCKALLVLGGDNEPDSEKSHRRKLSHFYVEKEEIG 172
 Db 1078 LRHVASKDAGVYTCLAQNTGGQVLCCKALLVLGGDNEPDSEKSHRRKLSHFYVEKEEIG 1137
 QY 173 RGVGFGFVVRVQHKNGKILCAKFIPLRSRTAQAYRERDILAAALSHPLVTGLDQFETRK 232
 Db 1138 RGVGFGFVVRVQHKNGKILCAKFIPLRSRTAQAYRERDILAAALSHPLVTGLDQFETRK 1197
 QY 233 TLILILELCSSEELLDRLYRKGVVTEAEVKVYIQQQLVEGLYHLHSHGVLRLDIKPSNIML 292
 Db 1198 TLILILELCSSEELLDRLYRKGVVTEAEVKVYIQQQLVEGLYHLHSHGVLRLDIKPSNIML 1257
 QY 293 VHPAREDIKICDFGPAQNTTPAELOFSQYGSPEFVSPEIIQQNPVSEASDIWANGVISYL 352
 Db 1258 VHPAREDIKICDFGPAQNTTPAELOFSQYGSPEFVSPEIIQQNPVSEASDIWANGVISYL 1317
 QY 353 SLTCSPPFAGESDRATILNLVLEGRVSWSSPMAHLSSEDAKDFIKATLQAPQAPSAQC 412
 Db 1318 SLTCSPPFAGESDRATILNLVLEGRVSWSSPMAHLSSEDAKDFIKATLQAPQAPSAQC 1377
 QY 413 LSHPWFLKSNPABEAHPINTKQLKFLARSRQWSILMSYKSLVWRSIPELIRGPDSPS 472
 Db 1378 LSHPWFLKSNPABEAHPINTKQLKFLARSRQWSILMSYKSLVWRSIPELIRGPDSPS 1437
 QY 473 LGVARHLCRDTGGSS 532
 Db 1438 LGVARHLCRDTGGSS 1497
 QY 533 AEASERSTEAPAPAPAPGEGPAAQGCYPRHSVLSLFYHQAGSPHGHGALAPGSRHRP 592

1498 AEASERSTEAPAPASPEGAPPAQCGVPRHSVIRSLFVHQAGESPEHCALAPGSRHRP 1557
593 ARRHLLKGGYIAGALPGLRPLMEHRVLEBEAAREEQATILLAKAPSFETALRLPASGTH 652
1558 ARRHLLKGGYIAGALPGLRPLMEHRVLEBEAAREEQATILLAKAPSFETALRLPASGTH 1617
653 LAPGSHSLHDSSTPRPSEACEAQRPLSPAGSAPGAPFIRDMGHPOGSKQLPSTGCHPG 712
1618 LAPGSHSLHDSSTPRPSEACEAQRPLSPAGSAPGAPFIRDMGHPOGSKQLPSTGCHPG 1677
713 TAQPERSPDSFWGQAPAPFCHPKGSAPOBQCSHPHAPVAPCPGSPFPQCKEAPLPVPS 772
1678 TAQPERSPDSFWGQAPAPFCHPKGSAPOBQCSHPHAPVAPCPGSPFPQCKEAPLPVPS 1737
773 PFLGQOAPAPAPAKASPLDLSKMGPDLSLPRGRKPGPCSPGASQASSQVSSLRVGS 832
1738 PFLGQOAPAPAPAKASPLDLSKMGPDLSLPRGRKPGPCSPGASQASSQVSSLRVGS 1797
833 SQVGTPEGPSLDAEGWTQAEADLSDSSTPTLQRPQEQVTMRKFSLGGRGVAGVAGYTGA 892
1798 SQVGTPEGPSLDAEGWTQAEADLSDSSTPTLQRPQEQVTMRKFSLGGRGVAGVAGYTGA 1857
893 FGGDAGGMLGQPMWARTAMAVSSEEEQEAAREASQSEQQEAREASPLQVARSARPVP 952
1858 FGGDAGGMLGQPMWARTAMAVSSEEEQEAAREASQSEQQEAREASPLQVARSARPVP 1917
953 EVGRAPTRSSPEPTFWEDIGQVSLVQIRDLSDGDAEADTISLDSVDPAYLNLSDLYDI 1012
1918 EVGRAPTRSSPEPTFWEDIGQVSLVQIRDLSDGDAEADTISLDSVDPAYLNLSDLYDI 1977
1013 KYLPPEFMI FRKVPKSAQPEPSPMAEELAEPEPTWPGELGPHAGLEITESESDVD 1072
1978 KYLPPEFMI FRKVPKSAQPEPSPMAEELAEPEPTWPGELGPHAGLEITESESDVD 2037
1073 ALLAAAVGRKKWSPPSRSLFHFPGRLPLDEPAELGLRERVKASVEHISRLKGRPEG 1132
2038 ALLAAAVGRKKWSPPSRSLFHFPGRLPLDEPAELGLRERVKASVEHISRLKGRPEG 2097
1133 LEKEGPRKPGLAGFRSLGKSWDRAPFTFLRELSDETVVLGOSVTLACQVSAQPAQAT 1192
2098 LEKEGPRKPGLAGFRSLGKSWDRAPFTFLRELSDETVVLGOSVTLACQVSAQPAQAT 2157
1193 WSKOGAPLESSESRVLISATLKNFQLLTILVVAEDLGVTTCVSNALGTVTITGVLRAKE 1252
2158 WSKOGAPLESSESRVLISATLKNFQLLTILVVAEDLGVTTCVSNALGTVTITGVLRAKE 2217
1253 RPSSEPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLEGSWTTLASDIFDCCLTSK 1312
2218 RPSSEPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLEGSWTTLASDIFDCCLTSK 2277
1313 LSRGTYTFRACVSKAGNPYSSEQVLLGGPSHLASEESQGRSAQPLPSTKTFAFQ 1372
2278 LSRGTYTFRACVSKAGNPYSSEQVLLGGPSHLASEESQGRSAQPLPSTKTFAFQ 2337
1373 TQIQGRFSVVRQCKEASGRALAAKIIPYHPKDKTAVLREYALKGLRHPHLAQLHAAY 1432
2338 TQIQGRFSVVRQCKEASGRALAAKIIPYHPKDKTAVLREYALKGLRHPHLAQLHAAY 2397
1433 LSPRHVLVLELCSGPPELLPCLAEASVSESKVYLWMLSATOYLHNOHLHLDLRSE 1492
2398 LSPRHVLVLELCSGPPELLPCLAEASVSESKVYLWMLSATOYLHNOHLHLDLRSE 2457
1493 NMIIETYNLLKVDLGNASQSLQEKVLPSEDKFDYLETNAPELLEGQGAQVPTDITWATGV 1552
2458 NMIIETYNLLKVDLGNASQSLQEKVLPSEDKFDYLETNAPELLEGQGAQVPTDITWATGV 2517
1553 TAFIMLSAEPVPSSEGDARDLQRLKGLVRLSRVAGLSGGAVAFIRSTLCAQPNRCA 1612
2518 TAFIMLSAEPVPSSEGDARDLQRLKGLVRLSRVAGLSGGAVAFIRSTLCAQPNRCA 2577
1613 SSCLOCPWLTEGPACSRPAPVTFTPTARLRVFNREKRALLYKRNLAQVR 1665

Db RESULT 4
ABG76187
ID ABG76187 standard; protein; 7968 AA.
XX
AC ABG76187;
XX
DT 09-MAY-2003 (first entry)
XX
DE Human serine/threonine or protein kinase 12599.
XX
KW Human; enzyme; serine/threonine kinase; protein kinase; 12599;
cardiovascular disease; heart failure; myocardial infarction;
blood vessel disorder; atherosclerosis; Kaposi's sarcoma; immunogen;
blood platelet disorder; thrombocytopaenia; leukaemia; Hodgkin's disease;
haemolytic anaemia; cellular proliferative disorder; cancer;
protein kinase disorder; autoimmune disorder; diabetes mellitus;
psoriasis; inflammatory bowel disease; rheumatoid arthritis;
multiple sclerosis.
XX
OS Homo sapiens.
XX
PN US2002168742-A1.
XX
PD 14-NOV-2002.
XX
PF 15-FEB-2002; 2002US-00077130.
XX
PR 15-FEB-2001; 2001US-0269201P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Kapeller-Libermann R, Acton SL;
XX
DR WPI; 2003-298729/29.
XX
N-PSDB; ABX11642.
XX
PT Novel isolated human protein kinase, designated 59079 or 12599
polypeptide, useful as diagnostic and therapeutic agents for preventing
cardiovascular diseases, proliferative disorders, and protein kinase
disorders.
XX
PS Claim 8; Page 84-104; 119pp; English.
XX
CC The invention relates to an isolated human serine/threonine or protein
kinase, 59079 or 12599 polypeptide, encoded by nucleic acid molecule
comprising at least 85% identity to the nucleic acids appearing as
ABX11641 and ABX11642 or their complement, a naturally occurring variant
of the kinases or their fragments. Also included are a non-human host
cell containing the nucleic acids, an antibody specific for the proteins,
identifying a compound which binds to the kinase (by contacting the
kinase or a cell expressing the kinase with a test compound and
determining whether the kinase binds to the test compound) and modulating
the activity of kinase using the identified compound. The kinases and
their encoding nucleic acids are useful as diagnostic and therapeutic
agents for preventing a disease or condition associated with an aberrant
or unwanted 59079 or 12599 activity in a subject, including
cardiovascular diseases such as heart failure, and myocardial infarction;
disorders involving blood vessels such as atherosclerosis, and Kaposi's
sarcoma; blood platelets disorder such as thrombocytopaenia, leukaemia,
Hodgkin's disease, haemolytic anaemia; cellular proliferative disorders
such as cancer; and protein kinase disorders such as autoimmune
disorders, diabetes mellitus, psoriasis, inflammatory bowel disease,
rheumatoid arthritis, and multiple sclerosis (many examples of diseases
and disorders are included in the specification). The kinases, their
encoding nucleic acids and antibodies are useful in screening assays,
detection assays (e.g. forensic biology), and predicting clinical trials and
diagnostic assays, prognostic assays, and monitoring clinical trials and
pharmacogenomics). The kinases and their encoding nucleic acids are
useful as query sequences to perform a search against public databases to
identify other family members or related sequences. The present sequence

PD	26-OCT-2000.
XX	
PF	11-APR-2000; 2000WO-US009488 .
XX	
PR	16-APR-1999; 99US-0129553P.
PA	(SCIO-) SCIOS INC.
XX	
PI	Zeng W, Stanton L, Kong H;
DR	WPI; 2001-007013/01.
XX	N-PSDB; AAC62287.
PT	Novel hlg5 polypeptides capable of regulating signal transduction and
PT	exhibiting kinase activity useful for identifying antibodies to treat
XX	cardiac diseases, and additional mediators of signal transduction.
PS	Claim 1; Page 68-74; 8ipp; English.
XX	
CC	The present sequence represents a splice variant of human in signal
CC	transduction polypeptide. The polypeptide is designated H19G5. The
CC	protein is capable of regulating signal transduction and exhibits kinase
CC	activity. The H19G5 transcript is expressed in the heart. H19G5
CC	polypeptides and polynucleotides are useful for preventing or treating a
CC	cardiac disease, such as congestive heart failure, dilated congestive
CC	cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy,
CC	mitral valve disease, aortic valve disease or tricuspid valve disease,
CC	angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary,
CC	arterial or thrombovascular hypertension, arteriosclerosis, atherosclerosis
CC	and cardiac tumours in humans. The polypeptide is also useful for
CC	detecting the expression of a protein capable of regulating signal
CC	transduction or the expression of a protein capable of acting as a donor
CC	or acceptor molecule of a phosphate group. The monoclonal antibodies can
CC	be used as probes for detecting discrete antigens expressed by tissue or
CC	cell samples, and therefore used in humans for localization and
XX	monitoring of microbial infection
SQ	Sequence 2596 AA;
	Query Match 96.3%; Score 8417; DB 4; Length 2596;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 1611; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	53 PPSMQVTIEDVQAOTGGTAQFEAIIEGDPPSPVTWKDSVQLVDSTRLSQQOEGTYSLV 112
Db	984 PPSMQVTIEDVQAOTGGTAQFEAIIEGDPPSPVTWKDSVQLVDSTRLSQQOEGTYSLV 1043
QY	113 LRHVASKDAGVYTCLAQNTGGQVLCKAEILLVGDNPEPSEKSHRRKLHGFYEVKEIG 172
Db	1044 LRHVASKDAGVYTCLAQNTGGQVLCKAEILLVGDNPEPSEKSHRRKLHGFYEVKEIG 1103
QY	173 RGVFGEVVRVGHKNKILCAAKTIPLRSRTRAQAYRERDI LAALSHPLVTGLLPQFTRK 232
Db	1104 RGVFGEVVRVGHKNKILCAAKTIPLRSRTRAQAYRERDI LAALSHPLVTGLLPQFTRK 1163
QY	233 TLIIILELCSSEELDLRLRKGVVVTEAEVKVIQQQLVEGLHYLHSHGVYHLHDIKPSNILM 292
Db	1164 TLIIILELCSSEELDLRLRKGVVVTEAEVKVIQQQLVEGLHYLHSHGVYHLHDIKPSNILM 1223
QY	293 VHPAREDKICDFGAQNITPABLOFSQYGSPBEFVSPEI IQONPVSEASDTWANGVISYL 352
Db	1224 VHPAREDKICDFGAQNITPABLOFSQYGSPBEFVSPEI IQONPVSEASDTWANGVISYL 1283
QY	353 SLTCSSPPAGESDRATLLNVLGRVSWSSPMAAHSEDADKF I KATLORAPQARFSAQC 412
Db	1284 SLTCSSPPAGESDRATLLNVLGRVSWSSPMAAHSEDADKF I KATLORAPQARFSAQC 1343
QY	413 LSHPWFLKSMFAEBAHINTKQLKFLIARSRWORSIMSKSLVMRSIPELLRGPPDSPS 472
Db	1344 LSHPWFLKSMFAEBAHINTKQLKFLIARSRWORSIMSKSLVMRSIPELLRGPPDSPS 1403
QY	473 LGVAHLCRDRTGGSSSSSSSDNELAPPFAKSLPPSVTHSFPLLHPGFLRPASLPFEE 532

QY 1613 SSCLOCPWLTBEGPACSRPAPVTFPTARLRFVVRNREKRALLYKHNLAQVR 1665
DB 2544 SSCLOCPWLTBEGPACSRPAPVTFPTARLRFVVRNREKRALLYKHNLAQVR 2596

RESULT 6
AAB85504
ID AAB85504 standard; protein; 1618 AA.
AC AAB85504;
XX 25-SEP-2001 (first entry)
XX Human protein kinase SGK145.
XX
KW Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human;
KW antiparkinsonian; virucide; antibacterial; antifungal; antimigraine;
KW analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;
KW antipsoriatic; antirheumatic; antiarthritic; ophthalmologic; anorectic;
KW osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic;
KW vasotropic; antidiabetic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200155356-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002337.
XX
PR 25-JAN-2000; 2000US-0178078P.
PR 31-JAN-2000; 2000US-0179364P.
PR 17-FEB-2000; 2000US-0183173P.
PR 17-MAR-2000; 2000US-0190162P.
PR 29-MAR-2000; 2000US-0193404P.
PR 13-NOV-2000; 2000US-0247013P.
XX
PA (SUGS-) SUGEN INC.
XX
PI Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX
DR WPI; 2001-476202/51.
DR N-PSDB; AAH46904.
XX
XX Kinase polypeptides useful for treating cancers, Alzheimer's disease,
XX viral infections, diabetes, obesity, organ transplant rejection and
XX rheumatoid arthritis.
XX
PS Claim 7; Page 215; 218pp; English.
XX
XX The invention provides human protein kinases and protein kinase-like
XX enzymes and polynucleotides encoding the polypeptides. The kinase
XX polypeptides and their modulators are useful for treating a disease or
XX disorder such as cancer, immune-related diseases, cardiovascular disease,
XX brain or neuronal-associated disease and metabolic disorders, including
XX cancers of tissues, cancers of hematopoietic origin, diseases of the
XX central nervous system, diseases of the peripheral nervous system,
XX Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic
XX lateral sclerosis, viral infections, infections caused by prions,
XX bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction,
XX mood disorders, attention disorders, cognition disorders, hypotension,
XX hyperextension, psychotic disorders, neurological disorders, dyskinesias,
XX metabolic disorders, and organ transplant rejection. They are also useful
XX for treating rhinitis, autoimmunity, atherosclerosis, psoriasis,
XX osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic
XX inflammatory bowel disease, rheumatoid arthritis, metabolic disorders
XX such as diabetes, obesity, cardiovascular diseases such as reperfusion
XX injury, coronary thrombosis, clotting disorders and atherosclerosis,
XX ocular diseases such as glaucoma, retinopathy and macular degeneration,
XX psychiatric and neurological disorders such as anxiety, schizophrenia,
XX dementia, manic depression, etc. The polynucleotides are useful in gene
XX therapy techniques to treat the above mentioned disorders. Sequences

CC	AAB85491-85522	represent the human protein kinases of the invention
XX		
SQ	Sequence 1618 AA;	
	Query Match 96.1%; Score 8403; DB 4; Length 1618;	
	Best Local Similarity 99.6%; Pred. No. 0;	
	Matches 1611; Conservative 0; Mismatches 1; Indels 6; Gaps 1;	
QY	54 PSMQVTTIEDVQAQCTGTAQFAIIIEGDPQPSVTVYKDSVQLVDSVTRLSQQQEGTTTSLVL 113	
DB	1 PSMQVTTIEDVQAQCTGTAQFAIIIEGDPQPSVTVYKDSVQLVDSVTRLSQQQEGTTTSLVL 60	
QY	114 RHVASKDAGVVTCLAQNTGGQVLCCKAELLVLG-----GDNEPDSEKSHRRKLHSFYEV 167	
DB	61 RHVASKDAGVVTCLAQNTGGQVLCCKAELLVLGAAASHSLGDNEDSEKSHRRKLHSFYEV 120	
QY	168 KEIICRGVGFVKVVOHKGKILCAAKFIPLSRKTRACAYREEDIIAALSHPLVTGLDQ 227	
DB	121 KEIICRGVGFVKVVOHKGKILCAAKFIPLSRKTRACAYREEDIIAALSHPLVTGLDQ 180	
QY	228 FETRTKLILILELCSSEELLDRLYRKGVVTEAEVKVYIQQLVEGLHYLHSHGVLDIKP 287	
DB	181 FETRTKLILILELCSSEELLDRLYRKGVVTEAEVKVYIQQLVEGLHYLHSHGVLDIKP 240	
QY	288 SNILMVHPAREDIKICDPFPAQNTTPAELOFSQVGSPEFVSPEIIQONPVSEASDIWAMG 347	
DB	241 SNILMVHPAREDIKICDPFPAQNTTPAELOFSQVGSPEFVSPEIIQONPVSEASDIWAMG 300	
QY	348 VISYLSLTCSPPFAGESDRATLLNVLEGRVSWSPMAAHLSEDAKOFIKATLQAPQARP 407	
DB	301 VISYLSLTCSPPFAGESDRATLLNVLEGRVSWSPMAAHLSEDAKOFIKATLQAPQARP 360	
QY	408 SAAQCLSHPWFLKSNPAEAEAHFINTKQLKFLARSWORSLSVYKSLVWRSIPPELLRGP 467	
DB	361 SAAQCLSHPWFLKSNPAEAEAHFINTKQLKFLARSWORSLSVYKSLVWRSIPPELLRGP 420	
QY	468 PDPSLGVARHLCDRTGSS 527	
DB	421 PDPSLGVARHLCDRTGSS 480	
QY	528 SLPEAEAEASERSTEAPAPSPAGAPPAAGCVPRHSVIRSLFYHQAGSPESHGALAPG 587	
DB	481 SLPEAEAEASERSTEAPAPSPAGAPPAAGCVPRHSVIRSLFYHQAGSPESHGALAPG 540	
QY	588 SRRHPARRHLLKGGYTAGALPGLREPLMEHRVLEEAAREEQATLLAKAPSETALRLP 647	
DB	541 SRRHPARRHLLKGGYTAGALPGLREPLMEHRVLEEAAREEQATLLAKAPSETALRLP 600	
QY	648 ASGTHLAPGHSHSLHSDSPSTPRPSSSEACGEAQLPSAPSGGAPIRDMGHGPGSKOLPST 707	
DB	601 ASGTHLAPGHSHSLHSDSPSTPRPSSSEACGEAQLPSAPSGGAPIRDMGHGPGSKOLPST 660	
QY	708 GGHGCTAQEPSPDSKMGQAPAPCHPKQGSAPQEGCSHPAVAPCPGSPFGSCKEAP 767	
DB	661 GGHGCTAQEPSPDSKMGQAPAPCHPKQGSAPQEGCSHPAVAPCPGSPFGSCKEAP 720	
QY	768 LVPSPFFLQGPAPAPAKASPPLDKSMGFGDISLFCRKPCKPCSPFGSASQASSQVSS 827	
DB	721 LVPSPFFLQGPAPAPAKASPPLDKSMGFGDISLFCRKPCKPCSPFGSASQASSQVSS 780	
QY	828 LRVGSSQVGTGPGSLDAEGTQAEADLSSTTLQRPQOVTMRKFSLGGRGYAGVAG 887	
DB	781 LRVGSSQVGTGPGSLDAEGTQAEADLSSTTLQRPQOVTMRKFSLGGRGYAGVAG 840	
QY	888 YGTAFAGDAGMVGQGMARIAMAWVSQSEEEQAEARAEASQSEEQBARAESPLPQVS 947	
DB	841 YGTAFAGDAGMVGQGMARIAMAWVSQSEEEQAEARAEASQSEEQBARAESPLPQVS 900	
QY	948 ARPVEVGRAPTRSSPEPTTWEDIGQVSLVQIRDLSDGDAEADTISLDSIVDPAVLNLS 1007	
DB	901 ARPVEVGRAPTRSSPEPTTWEDIGQVSLVQIRDLSDGDAEADTISLDSIVDPAVLNLS 960	
QY	1008 DLYDIKYLFFETMTFRKVPKSAQPEPPSPMAEELAEFPETWMPGCELGPHAGLEITEE 1067	

Db 961 DLYDIKYLPEFFMIFKVKPKAQPEPSPMAEELAEFPETWMPGELPHAGLSITEE 1020
 Qy 1068 SEDVDALLAAVGRKRKWSRSLFHPGRLPLDEPAELGLRERVKASVEHISILK 1127
 Db 1021 SEDVDALLAAVGRKRKWSRSLFHPGRLPLDEPAELGLRERVKASVEHISILK 1080
 Qy 1128 GRPEGLEKEGPRKPKQLASFLSLGLKSWDRAPTELRLSDTETVVLGQSVTLCAQVSAQP 1187
 Db 1081 GRPEGLEKEGPRKPKQLASFLSLGLKSWDRAPTELRLSDTETVVLGQSVTLCAQVSAQP 1140
 Qy 1188 AAQATWSKDCAPLESRRVLIISATLKNFOLLITLWVAEDIGVTCVSVALGTVTGTV 1247
 Db 1141 AAQATWSKDCAPLESRRVLIISATLKNFOLLITLWVAEDIGVTCVSVALGTVTGTV 1200
 Qy 1248 LRKAERPSSPCPDIGEVYADGVLLVWKPVSYSYGVTIVVQCSLEGGSWITLASDIFDC 1307
 Db 1201 LRKAERPSSPCPDIGEVYADGVLLVWKPVSYSYGVTIVVQCSLEGGSWITLASDIFDC 1260
 Qy 1308 YLTSKLSRGTYTFRACVSKAGMPYSPSEOVLLGSPHLSAEESSQGRSAQPLPSTK 1367
 Db 1261 YLTSKLSRGTYTFRACVSKAGMPYSPSEOVLLGSPHLSAEESSQGRSAQPLPSTK 1320
 Qy 1368 TFAFQTIQGRFVSVRQWCEKASGRALAAKIIIPYHPKDKTAVLRREYALKGLRHPLAQ 1427
 Db 1321 TFAFQTIQGRFVSVRQWCEKASGRALAAKIIIPYHPKDKTAVLRREYALKGLRHPLAQ 1380
 Qy 1428 LHAAYLSRHLVLIILELCSGPPELLCLAEARASYSESEVKYLMQMSATQYLHNOHILHL 1487
 Db 1381 LHAAYLSRHLVLIILELCSGPPELLCLAEARASYSESEVKYLMQMSATQYLHNOHILHL 1440
 Qy 1488 DLRSNNMITEXNLLKVDLGNALSOEKVLPDSKYNKYLETWVAPLEGGQAVPQTDI 1547
 Db 1441 DLRSNNMITEXNLLKVDLGNALSOEKVLPDSKYNKYLETWVAPLEGGQAVPQTDI 1500
 Qy 1548 WAIGVTAFTMLSAEYFVSSEGARDLQRLKGLVRLSRVAGLSGGAVAFRLSTLCAQPM 1607
 Db 1501 WAIGVTAFTMLSAEYFVSSEGARDLQRLKGLVRLSRVAGLSGGAVAFRLSTLCAQPM 1560
 Qy 1608 GRPCASSCLOCPWLEEGPACSRPAPVTFPTARLVFVRNREKRALLYKRNLAQVR 1665
 Db 1561 GRPCASSCLOCPWLEEGPACSRPAPVTFPTARLVFVRNREKRALLYKRNLAQVR 1618
 RESULT 7
 AAB30568
 ID AAB30568 standard; protein; 1610 AA.
 XX
 AC AAB30568;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE A full length human signal transduction polypeptide.
 XX
 KW Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;
 KW congestive heart failure; dilated congestive cardiomyopathy;
 KW hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;
 KW mitral valve disease; aortic valve disease; tricuspid valve disease;
 KW myocardial infarction; cardiac arrhythmia; arteriosclerosis;
 KW atherosclerosis; cardiac tumour; microbial infection.
 XX
 OS Homo sapiens.
 XX
 PN W0200063381-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009488.
 XX
 PR 16-APR-1999; 99US-0129553P.
 XX
 PA (SCIO-) SCIOS INC.
 XX

Zeng W, Stanton L, Kong H;
 WPI: 2001-007013/01.
 N-PSDB; AAC62286.

Novel h19G5 polypeptides capable of regulating signal transduction and
 exhibiting kinase activity useful for identifying antibodies to treat
 cardiac diseases, and additional mediators of signal transduction.

Claim 1; Page 61-65; 81pp; English.

The present sequence represents a human protein with putative function in
 signal transduction. The polypeptide is designated H19G5. The protein is
 capable of regulating signal transduction and exhibits kinase activity.
 The H19G5 transcript is expressed in the heart. H19G5 polypeptides and
 polynucleotides are useful for preventing or treating a cardiac disease,
 such as congestive heart failure, dilated congestive cardiomyopathy,
 hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve
 disease, aortic valve disease or tricuspid valve disease, angina
 pectoris, myocardial infarction, cardiac arrhythmia, pulmonary, arterial
 or renovascular hypertension, arteriosclerosis, atherosclerosis and
 cardiac tumours in humans. The polypeptide is also useful for detecting or
 the expression of a protein capable of regulating signal transduction or
 the expression of a protein capable of acting as a donor or acceptor
 molecule of a phosphate group. The monoclonal antibodies can be used as
 probes for detecting discrete antigens expressed by tissue or cell
 samples, and therefore used in humans for localization and monitoring of
 microbial infection

Sequence 1610 AA;

Query Match 96.1%; Score 8399; DB 4; Length 1610;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1608; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 56 MCVTTEDVQAGTGGTAQFAEIIIEGDPQPSVTWYKDSVQLVDSTRLSQOQGGTYSVLVLRH 115
 Db 1 MCVTTEDVQAGTGGTAQFAEIIIEGDPQPSVTWYKDSVQLVDSTRLSQOQGGTYSVLVLRH 60
 Qy 116 VASKAGVYTCIAQNTGGQVLCBAELLVLGGDNEPSEKSHRRKLMSPFVKEETGRGV 175
 Db 61 VASKAGVYTCIAQNTGGQVLCBAELLVLGGDNEPSEKSHRRKLMSPFVKEETGRGV 120
 Qy 176 FGFVVRVQHKGNKILCAAKFIFLRSRTAQAYRERDILAAALSHPLVTGLDQPETRKTLL 235
 Db 121 FGFVVRVQHKGNKILCAAKFIFLRSRTAQAYRERDILAAALSHPLVTGLDQPETRKTLL 180
 Qy 236 LILELCSSEELLDRLYRKGVTVEAKVYIQQVLEGLVHLHSHGVLEHLDKPSNITLWVHP 295
 Db 181 LILELCSSEELLDRLYRKGVTVEAKVYIQQVLEGLVHLHSHGVLEHLDKPSNITLWVHP 240
 Qy 296 AREDIKICDFGPAQNTIPAELOFSQYGSPEFVSPETIIQQNPFVSEASDIWAMGVISYLSLT 355
 Db 241 AREDIKICDFGPAQNTIPAELOFSQYGSPEFVSPETIIQQNPFVSEASDIWAMGVISYLSLT 300
 Qy 356 CSPPAGESDRATLLNVLEGRVSWSSPMAHLSEDAKDFIKATLQAPQAPRPSAAQCLSH 415
 Db 301 CSPPAGESDRATLLNVLEGRVSWSSPMAHLSEDAKDFIKATLQAPQAPRPSAAQCLSH 360
 Qy 416 PWFLLKMPAEAEAHFINTKQLKFLARSRWORSIMVSKSILVMSRISPELLRGPDSPSLGV 475
 Db 361 PWFLLKMPAEAEAHFINTKQLKFLARSRWORSIMVSKSILVMSRISPELLRGPDSPSLGV 420
 Qy 476 ARHLCRDTGGSS 535
 Db 421 ARHLCRDTGGSS 480
 Qy 536 SERSTEARPAPSPAGPAPPAQCVPRHSVIESLFWHONGESPHEGALARGSRHPPARR 595
 Db 481 SERSTEARPAPSPAGPAPPAQCVPRHSVIESLFWHONGESPHEGALARGSRHPPARR 540
 Qy 596 RHLLKGVYIAGALPGLREPLMEHVRLEEEAAREEQATLLAKAPSPETALURLPASGTHLAP 655

ID	Query Match	Best Local Similarity	Score	DB	Length
AA330567	standard; protein; 1351 AA.	80.9%;	7069;	DB 4;	Length 1351;
AA330567;		99.9%;	Pred. No. 0;		
19-MAR-2001	(first entry)	Mismatches 1;	Indels 0;	Gaps 0;	
AA330567	Amino acid sequence of a human signal transduction polypeptide.				
AA330567	Signal transduction; H19G5; kinase; cardiac disease; angina pectoris; congestive heart failure; dilated congestive cardiomyopathy; hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension; mitral valve disease; aortic valve disease; tricuspid valve disease; myocardial infarction; cardiac arrhythmia; arteriosclerosis; atherosclerosis; cardiac tumour; microbial infection.				
AA330567	Homo sapiens.				
AA330567	WO200063381-A1.				
AA330567	26-OCT-2000.				
AA330567	11-APR-2000; 2000WO-US009488.				
AA330567	16-APR-1999; 99US-0129553P.				
AA330567	(SCIO-) SCIOS INC.				
AA330567	Zeng W, Stanton L, Kong H;				
AA330567	WPI; 2001-007013/01.				
AA330567	N-PSDB; AAC62285.				
AA330567	Novel h19g5 polypeptides capable of regulating signal transduction and exhibiting kinase activity useful for identifying antibodies to treat cardiac diseases, and additional mediators of signal transduction.				
AA330567	Claim 1; Page 55-57; 81pp; English.				
AA330567	The present sequence represents a human protein with putative function in signal transduction. The polypeptide is designated H19G5. The protein is capable of regulating signal transduction and exhibits kinase activity. The H19G5 transcript is expressed in the heart. H19G5 polypeptides and polynucleotides are useful for preventing or treating a cardiac disease, such as congestive heart failure, dilated congestive cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve disease, aortic valve disease or tricuspid valve disease, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary, arterial or renovascular hypertension, arteriosclerosis, atherosclerosis and cardiac tumours in humans. The polypeptide is also useful for detecting the expression of a protein capable of regulating signal transduction or the expression of a protein capable of acting as a donor or acceptor molecule of a phosphate group. The monoclonal antibodies can be used as probes for detecting discrete antigens expressed by tissue or cell samples, and therefore used in humans for localization and monitoring of microbial infection.				
AA330567	Sequence 1351 AA;				
AA330567	Query Match	80.9%;	Score 7069;	DB 4;	Length 1351;
AA330567	Best Local Similarity	99.9%;	Pred. No. 0;		
AA330567	Matches 1348; Conservative	1;	Mismatches	1;	Indels 0; Gaps 0;
AA330567	316 LQFSQGSPPFVSPETIQNPVSEASDIWANGVIVSYLSITCSPSPAGESDRATLNVLEG	375			
AA330567	2 VQFSQGSPPFVSPETIQNPVSEASDIWANGVIVSYLSITCSPSPAGESDRATLNVLEG	61			
AA330567	376 RVSNSSPPMAHLSEDKDFIKATLQAPAPRSPAAQCLSHPWFLKSPAEAHFINTKQL	435			
AA330567	62 RVSNSSPPMAHLSEDKDFIKATLQAPAPRSPAAQCLSHPWFLKSPAEAHFINTKQL	121			
AA330567	436 KFLLRARWRQSLNYSKILVMSRIPPELLRGPPDPSPISLGVARHLCDRTGGSSSSSSSDN	495			
AA330567	132 KFLLRARWRQSLNYSKILVMSRIPPELLRGPPDPSPISLGVARHLCDRTGGSSSSSSSDN	181			

1576 LKGLVLSRCYAGLSGGAVAFRLSTLCAOPWGRPCASSCLQCPWLTEGPACSRPAPVT 1635
1262 LKGLVLSRCYAGLSGGAVAFRLSTLCAOPWGRPCASSCLQCPWLTEGPACSRPAPVT 1321
1636 FFAELRVFVRNREKRALLKRNLAQVR 1665
1322 FFAELRVFVRNREKRALLKRNLAQVR 1351
RESULT 9
AAE16274
ID AAE16274 standard; protein; 871 AA.
XX
AC AAE16274;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human kinase PKIN-20 protein.
XX
KW Human; kinase; PKIN-20; cancer; leukaemia; adenocarcinoma; osteoporosis;
immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
Acquired immune deficiency syndrome; AIDS; Addison's disease; anaemia;
allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
congestive heart failure; ischaemic heart disease; lung tumour; gout;
fatty liver; Niemann-Pick's disease; gene therapy.
XX
CS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 575..827
FT Domain /note="Eukaryotic protein kinase domain"
FT Domain /label="Protein_kinase_domain"
XX
PN WO200196547-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US019444.
XX
PR 15-JUN-2000; 2000US-0212073P.
PR 23-JUN-2000; 2000US-0213467P.
PR 30-JUN-2000; 2000US-0215651P.
PR 07-JUL-2000; 2000US-0216605P.
PR 13-JUL-2000; 2000US-0218372P.
PR 25-AUG-2000; 2000US-0228056P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
PI Gandhi AR, Tribouley JW, Walla NK, Yao MG, Lu DAM, Greenwald SR;
PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
XX
DR WPI; 2002-090207/12.
DR N-PSDS; AAD26467.
XX
PT New polypeptides, useful for diagnosing, treating or preventing disorders
of growth and development, cardiovascular and lipid, and diseases such as
cancer, comprise human kinase polypeptides.
XX
PS Claim 1; Page 164-165; 197pp; English.
XX
CC The invention relates to human kinase PKIN proteins and their
corresponding cDNAs. A composition containing PKIN agonist is useful for
treating a disease or condition associated with decreased expression of

496 ELAPFAKSLPPSPVTHSPLHPRGFLRPSASLPEEAASRSTEAAPPASPEGAGPP 555
182 ELAPFAKSLPPSPVTHSPLHPRGFLRPSASLPEEAASRSTEAAPPASPEGAGPP 241
556 AAGCCVPRHVSIRSLFTHQAGSEPHGALAPGSRHRRHLLKGGYIAGALPGLREPL 615
242 AAGCCVPRHVSIRSLFTHQAGSEPHGALAPGSRHRRHLLKGGYIAGALPGLREPL 301
616 MEHRVLEEAAREEQATLLAKAPSFETALRLPASGTHLAPGSHSLHSDSPSTPSSSEA 675
302 MEHRVLEEAAREEQATLLAKAPSFETALRLPASGTHLAPGSHSLHSDSPSTPSSSEA 361
676 CGENQRLPSAPSGAPIRDMGHPQGGKQIPSTGCGHGTGTAQPRPSPSPGWPAPAFCHPX 735
362 CGENQRLPSAPSGAPIRDMGHPQGGKQIPSTGCGHGTGTAQPRPSPSPGWPAPAFCHPX 421
736 QGSAPOEGGCSPHFAVAPCPGSPGSCKEAPLVPSSPFLGQOAPPAPAKASPLDLSKM 795
422 QGSAPOEGGCSPHFAVAPCPGSPGSCKEAPLVPSSPFLGQOAPPAPAKASPLDLSKM 481
796 GPGDISLPGPKGPCSSPGSASQASSQVSLRVGSSQVGTGPGPSLDAGTQAEADL 855
482 GPGDISLPGPKGPCSSPGSASQASSQVSLRVGSSQVGTGPGPSLDAGTQAEADL 541
856 SDSTPTLQRPQEQVTKRFTSLGGRGGYAGVAGYGTFAFGGDAGMGLGQGPWARIAMAVS 915
542 SDSTPTLQRPQEQVTKRFTSLGGRGGYAGVAGYGTFAFGGDAGMGLGQGPWARIAMAVS 601
916 QSEEEQEEARASQSEEEQEEARASPLQVGAARVPVEVGRAPTRSSPEPTFWEDIGQVS 975
602 QSEEEQEEARASQSEEEQEEARASPLQVGAARVPVEVGRAPTRSSPEPTFWEDIGQVS 661
976 LVQIRDLSGDAEAADTISLIDSEVDPAVNLNLDYDIKYLPEFMI FRKPKSAQPPPS 1035
662 LVQIRDLSGDAEAADTISLIDSEVDPAVNLNLDYDIKYLPEFMI FRKPKSAQPPPS 721
1036 PMAEELAEFPETPTWPGELGPHAGLEITESESDVDALLAAAVGRKRXKSSPSRSLFH 1095
722 PMAEELAEFPETPTWPGELGPHAGLEITESESDVDALLAAAVGRKRXKSSPSRSLFH 781
1096 FPCRHLPLDEPAELGLRERVKASVEHISRLIKRPEGLEKEGPPRKPGLASFLSLGLKS 1155
782 FPCRHLPLDEPAELGLRERVKASVEHISRLIKRPEGLEKEGPPRKPGLASFLSLGLKS 841
1156 WDRAPTFLRELSDETIVLQSVTLACQVSAQPAQAATWSKOGAPLESSSRVLI SATLKNF 1215
842 WDRAPTFLRELSDETIVLQSVTLACQVSAQPAQAATWSKOGAPLESSSRVLI SATLKNF 901
1216 QLLTILVVAEDLGVTCTSVNALGVTITGVLRAERPSPPSPCPDICEVYADGVLLVWK 1275
902 QLLTILVVAEDLGVTCTSVNALGVTITGVLRAERPSPPSPCPDICEVYADGVLLVWK 961
1276 PVESYGPVTIVQCSLEGGSWTTLASDIPDCCYLTSKLSRGTYTFRACVSKAGMPYS 1335
962 PVESYGPVTIVQCSLEGGSWTTLASDIPDCCYLTSKLSRGTYTFRACVSKAGMPYS 1021
1336 SPSEQVLLGGPSHLASEESQGRSAQPLPSTKTFAFQIQGRGFSVVRQCWKASGRAL 1395
1022 SPSEQVLLGGPSHLASEESQGRSAQPLPSTKTFAFQIQGRGFSVVRQCWKASGRAL 1081
1396 AAKIIPYHPKDTAVLREYEAUKGLRHPLAQLHAAYLSPRHLVLIILELCSGPELLPCLA 1455
1082 AAKIIPYHPKDTAVLREYEAUKGLRHPLAQLHAAYLSPRHLVLIILELCSGPELLPCLA 1141
1456 ERASYSESEVKDYLWQMLGATQVHLNQHILHLDLSENMITEYNLLKVDLGNASLSQ 1515
1142 ERASYSESEVKDYLWQMLGATQVHLNQHILHLDLSENMITEYNLLKVDLGNASLSQ 1201
1516 EKVLPDSKFKDYLETWAPLELGGQAVPQTDIWAIGVTAFIMLSABYVPSSEGARDLQRG 1575
1202 EKVLPDSKFKDYLETWAPLELGGQAVPQTDIWAIGVTAFIMLSABYVPSSEGARDLQRG 1261

PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, hepatocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, arteriosclerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease, osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's disease, rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts), cardio vascular disease (arteriovenous fistula, hypertension, vasculitis, aneurysms, congestive heart failure, angina pectoris, myocarditis, ischaemic heart disease, chronic bronchitis, lung tumours); lipid disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity of a test compound and in gene therapy. The present sequence is human PKIN-20 protein

Sequence 871 AA;
SQ

Query Match	51.9%	Score	4533	DB	5	Length	871		
Best Local Similarity	100.0%	Pred. No.	2.8e-277						
Matches	871	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	Qy	1	MGPGDISLPGRKPGPCSSPGSASQASSSQSSLRVGSQVGTGPGSLDAEGMTQAE	854					
Db	Db	1	MGPGDISLPGRKPGPCSSPGSASQASSSQSSLRVGSQVGTGPGSLDAEGMTQAE	60					
Qy	Qy	855	LSDSPTLQROEQVTKRKSLSGRGYAGVAGYGTFAFGDAGMGLQGPMWARIAMAV	914					
Db	Db	61	LSDSPTLQROEQVTKRKSLSGRGYAGVAGYGTFAFGDAGMGLQGPMWARIAMAV	120					
Qy	Qy	915	QSSEEEQEARAESQEEQEARAESPLQVSARPVPEVGRAPTRSSPEPTPWEDIGQV	974					
Db	Db	121	QSSEEEQEARAESQEEQEARAESPLQVSARPVPEVGRAPTRSSPEPTPWEDIGQV	180					
Qy	Qy	975	SLVQIRDLSDGAEADPTISLIDISEVDPAVNLSDLYDKYLPFFPMIRKVPKSAQPEPP	1034					
Db	Db	181	SLVQIRDLSDGAEADPTISLIDISEVDPAVNLSDLYDKYLPFFPMIRKVPKSAQPEPP	240					
Qy	Qy	1035	SPMAEELASFPETPWPMPGELGPHAGLITBESEDDVALLAEAAVGRKRWSPSRSLF	1094					
Db	Db	241	SPMAEELASFPETPWPMPGELGPHAGLITBESEDDVALLAEAAVGRKRWSPSRSLF	300					
Qy	Qy	1095	HFPGRHPLDEPABELGURERVKASVRHISRIILKGRPEGLEKGGPRKPGLASPLSGLK	1154					
Db	Db	301	HFPGRHPLDEPABELGURERVKASVRHISRIILKGRPEGLEKGGPRKPGLASPLSGLK	360					
Qy	Qy	1155	SWDRAPTLRELSDETVVLQGSVTLACQVSAQAAQATWSKDGAPLESSSRVLISATLKN	1214					
Db	Db	361	SWDRAPTLRELSDETVVLQGSVTLACQVSAQAAQATWSKDGAPLESSSRVLISATLKN	420					
Qy	Qy	1215	FOLLTILVVAEDLGVTCSVSNALGTVTITGVLRKAERPSSSPCPDIEGYVADGVLLVW	1274					
Db	Db	421	FOLLTILVVAEDLGVTCSVSNALGTVTITGVLRKAERPSSSPCPDIEGYVADGVLLVW	480					
Qy	Qy	1275	KPVESYGPVTIYVQCSLEGGSWTTLASDIPDCYITSLSRGGTYTFRATACVSRAGMPY	1334					
Db	Db	481	KPVESYGPVTIYVQCSLEGGSWTTLASDIPDCYITSLSRGGTYTFRATACVSRAGMPY	540					
Qy	Qy	1335	SSPSEQVLLGSPSHLASEESQGRSAQPLPSTKTFAQTQIQGRFVSVRQCKEKASGRA	1394					
Db	Db	541	SSPSEQVLLGSPSHLASEESQGRSAQPLPSTKTFAQTQIQGRFVSVRQCKEKASGRA	600					
Qy	Qy	1395	LAAXIIPYHPKOKTAVLRVEYALKGRHPLAQHLAAVLSPRHVLILEICSGPELLPCL	1454					
Db	Db	601	LAAXIIPYHPKOKTAVLRVEYALKGRHPLAQHLAAVLSPRHVLILEICSGPELLPCL	660					
Qy	Qy	1455	AERASYSSESEYKQYLMQWLSATQYLHNOHILHLDRSENMITTEYNLLKVVLDLGNAGLS	1514					

QY	1515	QEKVLPSDKFKDYLETMAPELLEGGGAVPQTDIWAIGTAFIMLSARYPVSSSEGADLQR	1570
Db	721	QEKVLPSDKFKDYLETMAPELLEGGGAVPQTDIWAIGTAFIMLSARYPVSSSEGADLQR	780
QY	1575	GLRKGLVRLSRVCYAGLSGGAVAFLESTLTCAPWGRPCASSCLOCPWLTETGSPACSRPAPV	1634
Db	781	GLRKGLVRLSRVCYAGLSGGAVAFLESTLTCAPWGRPCASSCLOCPWLTETGSPACSRPAPV	840
QY	1635	TFPTARLRFVFNREKRALLYKRNHQAQR	1665
Db	841	TFPTARLRFVFNREKRALLYKRNHQAQR	871
RESULT 10			
AAAB30570			
ID	AAAB30570	standard; protein; 871 AA.	
XX	AAAB30570;		
XX	19-MAR-2001	(first entry)	
XX	A splice variant of a signal transduction polypeptide.		
XX	Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;		
KW	congestive heart failure; dilated congestive cardiomyopathy;		
KW	hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;		
KW	mitral valve disease; aortic valve disease; tricuspid valve disease;		
KW	myocardial infarction; cardiac arrhythmia; arteriosclerosis;		
KW	atherosclerosis; cardiac tumour; microbial infection; splice variant.		
XX	Homo sapiens.		
OS	WO2000063381-A1.		
FN	26-OCT-2000.		
XX	11-APR-2000; 2000WO-US009488.		
PD	16-APR-1999; 99US-0129553P.		
XX	(SCIO-) SCIOS INC.		
XX	Zeng W, Stanton L, Kong H;		
PI	WPI; 2001-007013/01.		
XX	Novel h19G5 polypeptides capable of regulating signal transduction and		
PT	exhibiting kinase activity useful for identifying antibodies to treat		
PT	cardiac diseases, and additional mediators of signal transduction.		
PP	Claim 1; Page 74-76; 81pp; English.		
XX	The present sequence represents a splice variant of human in signal		
CC	transduction polypeptide. The polypeptide is designated H19G5. The		
CC	protein is capable of regulating signal transduction and exhibits kinase		
CC	activity. The H19G5 transcript is expressed in the heart. H19G5		
CC	polypeptides and polynucleotides are useful for preventing or treating a		
CC	cardiac disease, such as congestive heart failure, dilated congestive		
CC	cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy,		
CC	mitral valve disease, aortic valve disease or tricuspid valve disease,		
CC	angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary,		
CC	arterial or rheinovascular hypertension, arteriosclerosis, atherosclerosis		
CC	and cardiac tumours in humans. The polypeptide is also useful for		
CC	detecting the expression of a protein capable of regulating signal		
CC	transduction or the expression of a protein capable of acting as a donor		
CC	or acceptor molecule of a phosphate group. The monoclonal antibodies can		
CC	be used as probes for detecting discrete antigens expressed by tissue or		
CC	cell samples, and therefore used in humans for localization and		
CC	monitoring of microbial infection		
XX	Sequence 871 AA;		
XX	89		

XX	A full length rat signal transduction polypeptide.
DE	
KW	Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;
KX	congestive heart failure; dilated congestive cardiomyopathy;
KW	hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;
KV	mitral valve disease; aortic valve disease; tricuspid valve disease;
KW	myocardial infarction; cardiac arrhythmia; arteriosclerosis;
KW	atherosclerosis; cardiac tumour; microbial infection.
OS	Rattus norvegicus.
XX	
PN	WO20063381-A1.
PD	26-OCT-2000.
XX	
PX	11-APR-2000; 2000WO-US009488.
XX	
PR	16-APR-1999; 99US-0129553P.
XX	(SCIO-) SCIOS INC.
PA	Zeng W, Stanton L, Kong H;
PI	WPI; 2001-007013/01.
DR	
XX	
PT	Novel h19G5 polypeptides capable of regulating signal transduction and
PT	exhibiting kinase activity useful for identifying antibodies to treat
PT	cardiac diseases, and additional mediators of signal transduction.
XX	
PS	Claim 1; Page 76-77; 81pp; English.
XX	
CC	The present sequence represents a rat signal transduction polypeptide,
CC	designated R19G5. The human polypeptide is designated H19G5. The protein
CC	is capable of regulating signal transduction and exhibits kinase
CC	activity. The H19G5 transcript is expressed in the heart. H19G5
CC	polypeptides and polynucleotides are useful for preventing or treating a
CC	cardiac disease, such as congestive heart failure, dilated congestive
CC	cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy,
CC	mitral valve disease, aortic valve disease or tricuspid valve disease,
CC	angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary,
CC	arterial or renovascular hypertension, arteriosclerosis, atherosclerosis
CC	and cardiac tumours in humans. The polypeptide is also useful for
CC	detecting the expression of a protein capable of regulating signal
CC	transduction or the expression of a protein capable of acting as a donor
CC	or acceptor molecule of a phosphate group. The monoclonal antibodies can
CC	be used as probes for detecting discrete antigens expressed by tissue or
CC	cell samples, and therefore used in humans for localization and
CC	monitoring of microbial infection
XX	
SQ	Sequence 548 AA;
XX	
Query Match	28.0%; Score 2447.5; DB 4; Length 548;
Best Local Similarity	86.4%; Pred. No. 7.6e-146;
Matches	472; Conservative
	27; Mismatches 46; Indels 1; Gaps 1;
QY	1121 HISILKRGEGLEKEGPKRKPLASFRSLGLKSWDRAPFLRELSDTVVLQGVSITLA 1180
Db	3 HISILKKGEGEKGPKRKPLASFRSLGLKGRDQAPFLRELSDAEVVLQGSVTLA 62
QY	1181 QVSAQAQAATWSKDGAPELSSSRVLISATLNKFNQLLTILLVAEDLVGVYTCSVSNALG 1240
Db	63 QCVLAQTAQTWSKDGAELLESSGHLLISSTLNKFNQLLTILLVTEEDLGTYTCVSNPLG 122
QY	1241 TVTTTGVLRKAEPSSSPCPDGEVVADGVLLVMKPVSRYGPVTIVOCLESLEGGSWTTLA 1300
Db	123 TAVTTGVLRKAEPSSPREVEGELYTDALLVMKPVSRYGPVTIVOCCLIEGGSWTTLA 182
QY	1301 SDIPDCCYLTSLKSROGTTFRTACVSKAGMGFYPSSPEQVLGGPSHLASEEP-SGGRS 1359
Db	183 SDISDCCYLTGKLPGGMWTFRTACVSKAGMGFYPSSPEQVLGGPNHLEASEESSRGRP 242
QY	1360 AQLPFSKTFAFTQIQGRGFYSVRQCWEKASGRALAALKIIPYHPKDKTAVLREYALKG 1419

Db 243 AQLPSTKTFATQIRGRFSVVRQCRKASGRALAAKIVPYQEDKTVLREYALKR 302
 QY 1420 LHPHPLAQLHAAYLSPRHLVILILELCSGPPELLPCLAEASYSSESEKDYLMQMLSATQYL 1479
 Db 303 LHPHPLAQLHAAYLSPRHLVILILELCSGPPELLPCLAEASYSSESEKDYLMQMLSATQYL 362
 QY 1480 HNOHILHLDLRSENMIITEYNLLKVDLGNQAQSLSEKVLPSDKFKDYLETWAPLLEGG 1539
 Db 363 HAQHILHLDLRSENMMVTENLLKVIDLGNQAQSLSEKVKYLETWAPLLEGG 422
 QY 1540 GAVPQTDIWAIGTAFIMLSAEYFVSEGGARDLQGRGLKGLVRLSRVAGLSGGAVAFLR 1599
 Db 423 GAVPQTDIWAIGTAFIMLSAEYFVSEGGARDLQGRGLKGLVRLSRVAGLSGGAVAFLR 482
 QY 1600 STLCAQPMGRPCASSCLQCPMLTEEGPACSRPAPVPTPTARLRFVVRNKRKRALLYKXH 1659
 Db 483 SSLCAQPMGRPCASTCLQCGMLTEEGTGSRTPTPTPTARLRFVVRNKRKRALLYKXH 542
 QY 1660 NLAQVR 1665
 Db 543 NLAQVR 548

RESULT 12

AAB30572

ID AAB30572 standard; protein; 548 AA.

XX AC AAB30572;

XX DT 19-MAR-2001 (first entry)

XX DE A full length mouse signal transduction polypeptide.

XX KW Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;
 KW congestive heart failure; dilated congestive cardiomyopathy;
 KW hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;
 KW mitral valve disease; aortic valve disease; tricuspid valve disease;
 KW myocardial infarction; cardiac arrhythmia; arteriosclerosis;
 KW atherosclerosis; cardiac tumour; microbial infection.

XX OS Mus musculus.

XX PN WO200063381-A1.

XX PD 26-OCT-2000.

XX PF 11-APR-2000; 2000WO-US009488.

XX PR 16-APR-1999; 99US-0129553P.

XX PA (SCIO-) SCIOS INC.

XX PI Zeng W, Stanton L, Kong H;

XX PS WPI; 2001-007013/01.

XX CC Novel h19G5 polypeptides capable of regulating signal transduction and
 PT exhibiting kinase activity useful for identifying antibodies to treat
 PT cardiac diseases, and additional mediators of signal transduction.
 XX PS Claim 1; Page 77-79; 81pp; English.

XX CC The present sequence represents a mouse signal transduction polypeptide,
 CC designated M19G5. The human polypeptide is designated H19G5. The protein
 CC is capable of regulating signal transduction and exhibits kinase
 CC activity. The H19G5 transcript is expressed in the heart. H19G5
 CC polypeptides and polynucleotides are useful for preventing or treating a
 CC cardiac disease, such as congestive heart failure, dilated congestive
 CC cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy,
 CC mitral valve disease, aortic valve disease or tricuspid valve disease,
 CC angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary,
 CC arterial or rheonovascular hypertension, arteriosclerosis, atherosclerosis

CC and cardiac tumours in humans. The polypeptide is also useful for
 CC detecting the expression of a protein capable of regulating signal
 CC transduction or the expression of a protein capable of acting as a donor
 CC or acceptor molecule of a phosphate group. The monoclonal antibodies can
 CC be used as probes for detecting discrete antigens expressed by tissue or
 CC cell samples, and therefore used in humans for localization and
 CC monitoring of microbial infection

XX SQ Sequence 548 AA;

Query Match 27.6%; Score 2415.5; DB 4; Length 548;

Best Local Similarity 85.7%; Pred. No. 8e-144;

Matches 468; Conservative 25; Mismatches 52; Indels 1; Gaps 1;

QY 1121 HHSRLIKGRPGLEKEGPRKPKGLASFRLSGLSKMDRAPTEFLRSDETVVLGQSVTLA 1180

Db 3 HHSRLIKGRPGLEKEGPRKPKGLASFRLSGLSKMDRAPTEFLRSDETVVLGQSVTLA 62

QY 1181 QVNSAQPAQAQTSKDGAPLESSEKSVLISATLKNFQLLTILVVVAEDLGVYTCVSNALG 1240

Db 63 CQVLAQTAQATWSKDGVLSESGHLLISLTKNFQLLTILVVKEEDLGTTCVSNPLG 122

QY 1241 TVTTTGVLRKKAERPSSPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLEGGSWTTLA 1300

Db 123 TAVTTGVLRKKAERPSSPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLEGGSWTTLA 182

QY 1301 SDIFPCCVLTSLSRGTYTFRACVSKAGMGYSSEQVTLGGPSHLASEE-SQGRS 1359

Db 183 SDISDCVLTSLSRGTYTFRACVSKAGMGYSSEQVTLGGPSHLASEE-SQGRS 242

QY 1360 AQLPSTKTFATQIRGRFSVVRQCRKASGRALAAKIVPYQEDKTVLREYALKR 1419

Db 243 AQLPSTKTFATQIRGRFSVVRQCRKASGRALAAKIVPYQEDKTVLREYALKR 302

QY 1420 LHPHPLAQLHAAYLSPRHLVILILELCSGPPELLPCLAEASYSSESEKDYLMQMLSATQYL 1479

Db 303 LHPHPLAQLHAAYLSPRHLVILILELCSGPPELLPCLAEASYSSESEKDYLMQMLSATQYL 362

QY 1480 HNOHILHLDLRSENMIITEYNLLKVDLGNQAQSLSEKVLPSDKFKDYLETWAPLLEGG 1539

Db 363 HAQHILHLDLRSENMMVTENLLKVIDLGNQAQSLSEKVKYLETWAPLLEGG 422

QY 1540 GAVPQTDIWAIGTAFIMLSAEYFVSEGGARDLQGRGLKGLVRLSRVAGLSGGAVAFLR 1599

Db 423 GAVPQTDIWAIGTAFIMLSAEYFVSEGGARDLQGRGLKGLVRLSRVAGLSGGAVAFLR 482

QY 1600 STLCAQPMGRPCASSCLQCPMLTEEGPACSRPAPVPTPTARLRFVVRNKRKRALLYKXH 1659

Db 483 SSLCAQPMGRPCASTCLQCGMLTEEGTGSRTPTPTPTARLRFVVRNKRKRALLYKXH 542

QY 1660 NLAQVR 1665

Db 543 NLAQVR 548

RESULT 13

AAB65635

ID AAB65635 standard; protein; 2286 AA.

XX AC AAB65635;

XX DT 27-MAR-2001 (first entry)

XX DE Novel protein kinase, SEQ ID NO: 162.

XX KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antidiabetic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.

XX OS Homo sapiens.

XX	WO200073469-A2.
PN	
XX	
XX	07-DEC-2000.
XX	
XX	26-MAY-2000; 2000WO-US014842.
XX	
PF	
XX	28-MAY-1999; 99US-0136503P.
PR	
XX	(SUGE-) SUGEN INC.
XX	
PI	Plowman GB, Martinez R, Whyte D, Sudersanam S;
XX	
XX	WPI; 2001-032161/04.
DR	
DR	N-PSDB; RAFP4662.
XX	
XX	
PT	Nucleic acids encoding kinase polypeptides, useful
PT	treating immune-related diseases and disorders, c
PT	neurodegenerative diseases and/or cancers.
XX	
XX	Claim 10; Fig 1; 310pp; English.
PS	

The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression and such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.

Sequence 2286 AA;

Query Match 22.6%; Score 1973; DB 4; Length 2286;

Best Local Similarity 29.3%; Pred. No. 5.3e-115;

Matches 568; Conservative 236; Mismatches 638; Indels 498; Gaps 50;

QY 54 PSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWKDSVQLVDSTRLSQQQEGTYSVL 113

504 PRFESIMEDVEVGAGETARFAVVEGKPLPDIMWKDEVLLTTESSHVSFVYEENECSLW 563

114 RHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDN-----EPDSEKOSHR-RKLHSFYEVK 168

564 LSTGAODGGVYTCTAONLAGEVSCKAELA VHS AOTAMEVEGVGEDEDEHRCGRRI.SDFYDTH 623

169 EETGRGVEGEVKRVQHKGNKII.CAAKFPI.RSPTBAQAYPERDII.AAISHPI.YTCII.DOE 328

624 0E1CBGAPESVI PPIVETPSSCI PBAAYET PSCAYDVA SAPPBEPDI TAPY OUDCT YETIENAP 503

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(The page contains musical notation consisting of staves with notes.)

[illegible][illegible][illegible]

QZ 347 30VIL02UC1C35EFA0ESDUNAJUNVDEKVSWSSEFATLSESDANDF-INAIUQAPQA 403

DD 803 GVVAFDCLIGISFFVGENDRIILMNIRKYNVAFEEITFLSLSRKARGFTIKVLVQ--DRL 860

406 RPSAAQCLSHPPWFLKSMPEAEAAFFINTKQLKFFLLARSRWQSLMSYKSLVMRSIPELLR 465

DB 861 RPTAETLEHPWFKTQAKGAE--VSTDHLKFLSRRRWQRSQISYKCHLVLRPIPELLR 917

QY	466	GPPDPSLGVARHLCDRTDGGSSSSSSSSSDEL-----APPAPAK-SLPSPFVTH	513
Db	918	PPERVVWMPBR-PPPSSGLSSSDSEEELEELPSPRPRLQPFGSGRSLTDIPTED	976
QY	514	SPLLHPRGFLRSASLPEAEAEASERSTAPAPASPAGPAGPAQAQCVPRHVSIR----	568
Db	977	EALGTPETGAATMDWQEGRAPSQDQEAPSFEALPSPQCEPAA-CASPRCELARGSSA	1035
QY	569	-----SLFYHQAG--ESEHGALADP-----SRHPRARRHLIK	600
Db	1036	ESALPRAGPRELGRGLHKAAVSVELPORRSPGPGATLARGGLGEYAFORLOALQRLLR	1095
QY	601	GGYTAGALPGLREPLMEH-----RVUEEAAREEQATL-----LAKAPSFETALR	645
Db	1096	GGPEDKSVLRGPPLLESILGGRARDPRMARAAASSEAPHQPLENRGLQKSSFSQGEA	1155
QY	646	LPASTCHLAPGHSHLSIHDSPSTPR-----PSSEACGEARQLPSASPAGPIRDMGHPQS	701
Db	1156	EP-RGRHRRAGALDEIVARLGARLQSPSUSALSEAQ--DSSFA-----RPSAP	1203
QY	702	KOLPSTGGHPGTQAPERPSPOSPWGQAPPFCHPKQGSAPQEGCSPHPAVAPCPGSPFRG	761
Db	1204	K-PST--PKSAEPSAUTPTSDAPOPPAP--OPAOBKAPEPEPEPVRAASKPAP---PPQ	1252
QY	762	SCK--EAPLVPSPPFQG-----PQAPPAPAK-----ASPPLDSKMGP	797
Db	1253	ALQTIALPLTPTVAQIIQSLUSGHAGQSGQPAAPPSEPKHAUAVPARVASPP-----	1305
QY	798	GDISLPGRPKPGCGPCSGSAGOASSVSSLRVGSSQVGTPEGPSLDABGMTQEADLSD	857
Db	1306	----PGAPEKRVPSAGGPPVLAEARVPT-----VPPRPGSSLSSSIENLESEAVEF	1353
QY	858	SPTTLQRQCEQVTMRKFSLGGRGGYAGVAGYGTTFAGDGAGMLCQGPWWARIAVQSOS	917
Db	1354	A--KFKRGRES-----PLSLGLR-----LLERS	1374
QY	918	EEEEQEER-ABSQEEEOEARAESPLQVSAVPVEVGRATRSPSEFTPMWDIGQVSL	976
Db	1375	RSEERGFRGAEEEDGIYRSPAGTFL-----ELVRPERSR-----	1411
QY	977	VOIRDLS--GDAEAADTTSLDISVDPAYNLSDLUYDKILPFEBMIFRKVPKSAQBEPP	1034
Db	1412	-SVQDLRAVGEPGLVRLSLSLSQ-----RLRPTPAQR-----	1444
QY	1035	SPMAEELAEFPPEPTWMPBELGPHAGLEITESESDVDALLAEAANGKRKW-----	1086
Db	1445	-----HPAWAERAGDQ-----ESSEGSSARGSPVLAMRRRLSFTLERLS	1484
QY	1087	----SSPSRSILFHPGGRHLPDEPAELGLRERVKASVEHILSRILKGPP-----	1130
Db	1495	RELQRSGSSESUGSAGHSTFL-----FGRLRATSEGESLRLL--GLPHQLAAQAGAT	1537
QY	1131	-----EGLEKEGP-----PRKKPGLASFRLSG-----LK	1154
Db	1538	TPSAESLSEASATSGSAPGESRSLRWGFSRPRKDGLPNNLSASVBQELGHQYVRS	1597
QY	1155	SWDRAPTFLRELSDBTVVLGOSVTLAQCVSPAQAATWSXDGAFILESSSRVLI SATLKN	1214
Db	1598	BSDFFPVTHIKDOVILEGEANTLLCLPACPAPHISWMKDKXSLRSEPSVII VSCKDQ	1657
QY	1215	FOLLITLVVABDLGVYTCVSYNALGVTVTGTVLRKAERPSSSPCDTIGEVIADVLLW	1274
Db	1658	ROLLSIPRAGRHRHAGLYBCSATNVLGSISSCTVAVARVPKLAAPPEVTQTYQDTALVM	1717
QY	1275	KPVESYGVPVTI VQCSLEBGS-WTTLASDI PDCCVLTSKLGRGGTYTERTACVSKAGMP	1333
Db	1718	XPGDSRACVTTLERRVDGESVWHPVSGIIDFCYINVNTHLPVGVTVRFVACANRAGQGP	1777
QY	1334	YSSPSESQVLLQG-----	1345
Db	1778	FSNSSEKYFVRGTQDSSAVPSAAHQEAPVTSRPARPPDPSTSLAPLAPAAPTPPSVT	1837

QY 1346 -----PSHLSEESQSG-----RSAQP-LPST----- 1366
 Db 1838 VSPSPPTPPSOALSSKAVGPPPTPRRHRGLQARPAEPTLPSTHTPSEPFPVLVD 1897
 QY 1367 ----- 1366
 Db 1898 TGTPIASTPGQVPRVSSSTFVVVTSFVSAPAPAPPEPPPEPTKTVQVSLSPAKEV 1957
 QY 1367 -----KTFATQIQIGRFSVVRQCKEASGRALAAKIP 1401
 Db 1958 VSSPOSSPRSPREGTTLRQGPQKPYTFLEKARGRFGVVRACRENATGTFTVAKIYP 2017
 QY 1402 YHPKDKTAVJREYALKRHLPHLAQAAAYLSPRHVLVILELCSPELLPCLAEASYS 1461
 Db 2018 YAAEGKPRVLOEYEVLRITLHHRIMSLHEAVITPRVILVIAESCGNRELLGLSDRFRYS 2077
 QY 1462 ESEVKDYLWOMLSATOVLEHQHILHDLRSENMITEYLLKVDLGNASQSKVLP 1521
 Db 2078 EDVATYVWQLGLDYLHGHVHLZDKPDNLLLPADNALKIVDFGSAQFYNPQALRPL 2137
 QY 1522 DKFDYLETMAPELLEGQAVPTDIWAIGTAFIMLSAEYFVSSSEGARDLQGRKGLV 1581
 Db 2138 CHRTGTFLEFMAPEVVKGEPIGSAITDINGAGVLTVMILSGRSPFYPEDPQETEARIVGGRF 2197
 QY 1582 RLSRCYAGLSGAVAFRLSTLCQPMGRPCASSCLOCPMLTEGFPACSPAPVTFPTARL 1641
 Db 2198 DAFQLYPNTSOSATFLKVLVSHFWRPSLQDCLAHPLQDLYMLKURQTLTFTTNRL 2257
 QY 1642 RVFVNRKRRALYKHNL 1661
 Db 2258 KEFLGEQRRRAEAATRHV 2277
 RESULT 14
 ID AAE19160 standard; protein: 2380 AA.
 AC AAE19160;
 DT 21-MAY-2002 (first entry)
 DE Human kinase polypeptide (PKIN-18).
 KW Human; kinase polypeptide; PKIN-18; gene therapy; Addison's disease;
 KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
 KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
 KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
 KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
 KW cholestasis; cardiac; cardiovascular disorder; Niemann-Pick's disease;
 KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
 KW drug screening; transgenic animal; anti-inflammation; hepatotropic;
 KW hypotensive; anti-HIV; enzyme.
 OS Homo sapiens.
 FH Key
 FT Peptide 52..70 Location/Qualifiers
 FT Protein 71..2380 /label= Signal_peptide
 FT /note= "Mature human PKIN-18"
 FT Domain 714..967 /note= "Eukaryotic proetin kinase domain"
 FT Domain 2079..2331 /note= "Eukaryotic proetin kinase domain"
 XX WO200208399-A2.
 PN 31-JAN-2002.
 PD 20-JUL-2001; 2001WO-US023092.
 XX 21-JUL-2000; 2000US-0220038P.
 PR 28-JUL-2000; 2000US-0222112P.
 PR

PR 04-AUG-2000; 2000US-0222831P.
 PR 11-AUG-2000; 2000US-0224729P.
 XX (INCY-) INCYTE GENOMICS INC.
 PA (THOR/) THORNTON M.
 XX Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK,
 PI Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
 PI Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;
 PI Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DM, Greenwald SR;
 PI Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
 XX WPI; 2002-206083/26.
 DR N-PSDB; AAD30565.
 XX New human kinase polypeptide, useful in diagnosis, prevention and
 PT treatment of cancer, immune disorder, growth and developmental disorder,
 PT cardiovascular disorder and lipid disorder.
 XX Claim 1; Page 163-168; 196pp; English.
 XX The present invention relates to an isolated human kinase polypeptide
 CC (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
 CC useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
 CC lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
 CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
 CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
 CC bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
 CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
 CC infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
 CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
 CC drug screening techniques and to analyse the proteome of a tissue or cell
 CC type. PKIN is useful for creating knockin humanised animals or transgenic
 CC animals to model human diseases, in somatic or germline gene therapy, to
 CC generate a transcript image of a tissue or cell type, for detecting
 CC differences in the chromosomal location due to translocation, inversion,
 CC etc., among normal, carrier or affected individuals, and as hybridisation
 CC probes for mapping naturally occurring genomic sequences. PKIN is useful
 CC in southern or northern analysis, dot blot or other membrane-based
 CC technologies, in PCR technologies, in dipstick, pin, multiformat enzyme
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
 CC fluids or tissues from patients to detect altered PKIN expression. The
 CC present sequence is human PKIN-18. Note: This sequence is said to be
 CC encoded by PKIN-18 cDNA referred as SEQ ID NO:38 (AAD30565). However this
 CC does not appear to be the case
 XX Sequence 2380 AA;
 SQ Query Match 22.6%; Score 1973; DB 5; Length 2380;
 Best Local Similarity 29.3%; Pred. No. 5,7e-115;
 Matches 568; Conservative 236; Mismatches 638; Indels 498; Gaps 50;
 QY 54 PSMQVTTEDVQAGTGAQFEALIEGDPQPSVTWYKDSQVLDVSTRLSQOQEGTYSVLV 113
 Db 598 PRFESIMEDVEVGAGETARFAVVVEGKPLDPMWYKDEVLTTESHSVYFENECSLVV 657
 QY 114 RHVASKDAGVYTTCLAQNTGGQVLCKAEALLVGLGDN---EPDSEKQSHR-RKLHSPFYEK 168
 Db 658 LSTGAQDGGVYVTCQAQNLAGEVSKAEALVHSAQTAMEVGVGDEDEHGRSLSDFYDIH 717
 QY 169 BEIGRGVGFVKVQHKGNILCAAKFIPLRSTRACQAYRERDILAAALSHPLVTGLDQF 228
 Db 718 QEIGRGAFSYLRIRIVERSSGLEFAAPFIPQAKPKASRREARLARLOHDCULFHEAP 777
 QY 229 ETRKTLILILELCSSELLDRLYRKGVTTEAEVKKYIQQLVEGLHYLHSHGLHLDIKPS 288
 Db 778 ERRRLGLVITELC-TEBLERIAKPTVCBSERAYMRQVLEGIHYLHSHGLHLDVKPE 836
 QY 289 NILMVHPA--REDIKICDFGAQNIIPAELOFSQVGSPEFVSPEIIOQNPVSEADINAM 346
 Db 837 NLLVWDGAGEQVRIICDFGNAGELTPGEPOYQYGTPEFVAFEPVQSPVSGVTIDIFV 896
 QY 347 GVISVLSLTCSSPPAGESDRATLLNLEGRVSWSPMAAHLSEDAKDF-IKATLQRAPOA 405

Db 897 GWVAFCLTGISPVGENDRTLLMIRNYNAFEETTLFLSREARGFLIKVLQ--DRL 954
Qy 406 RPSAQCCLSHPWFLKSPASEAHFINTKQKFLAASRWORSIMSKSLVMRESIPELIR 465
Db 955 RPTAEETLEHPWFTQAKGAE---VSDHLKLFSSRRWORSOISYKCHLVKRPPELIR 1011
Qy 466 GPPDSPSLGVARHLCRTDGTSSSSSSSSDNEL-----APPARAK-SLPPSPVTH 513
Db 1012 APPERVVMTFPR--PPSPGGLSSSSSEELBELSPVRPLQPEPSGRSVLTDIPTED 1070
Qy 514 SPLHPRGFLRPSASLPEEAERSTAPAPPASPEGAGPPAAQCVPRHVSIR----- 568
Db 1071 EALGTPTGATPMDWCEQGRASPQOEAPSPALFSPQOEPA--GASPRRELARGGSA 1129
Qy 569 -----SLFYHQAG--ESPEHGALAPG-----SRHPARRHLLK 600
Db 1130 ESALPRAGPRELGLGKHAASVELPQRRSPGPGATLARGGLGEGEYQRLQALQRLIR 1189
Qy 601 GGYTAGALPGLREPLMEH-----RVLEBAAREEQATL-----LAKAPSPETALR 645
Db 1190 GGPEDGVSGULRGLLESGLGRARDPRMARAAASEAAPHQPPLENRGLQKSSFSQGEA 1249
Qy 646 LPASGTHLAPGHSLSLHDSFSTPR-----PSSBACGEAQLRSPASGGGAPIRDMGHPOGS 701
Db 1250 EP-RGRHRRAGAPLEIIVARLGAARRLQESPSLSALSEAQ--PSSPA-----RPSAP 1297
Qy 702 KQLPSTGCHGCTAOPERPSPDPMGQAPPCFKPGKQSAPOEGCSHPAVAPCPGSPFPG 761
Db 1298 K--EST--PKSAEFSATTESDAPQPPAP--QAQDKAFEPPEPVRASKPAP-----PPQ 1346
Qy 762 SKC--EAPLVSPSPFLOQ-----POAPPAPAK-----ASPPDSKMGVP 797
Db 1347 ALQTLALPLTPYAQIIQSLQSLGHAQPSQGPAPPEPSEPKPAAPVAVASPP----- 1399
Qy 798 GDISLPGRPKPGPCSPGSAQSSQSVSLRVSGSQVGTQPCPSLDAEGWTOEADLSD 857
Db 1400 -----PGAPEKVPASGPPVLEAKAVPT-----VPPRGOSSLSSENLESEAVFE 1447
Qy 858 STPTLQRPQEQVTKRPSLGRGGYAGVAGYGTFAFGDAGGMLGQGPMMARIAWAVSQS 917
Db 1448 A--KFKRSRES-----PLSLGLR-----LLSRS 1468
Qy 918 EEECEEAR--AESQSEEQGARAESPLPQVSARVPVEVGRAPTRSPSEPTPWEDIGQVSL 976
Db 1469 RSEERGFGRGAEEDGYRSPAGTPL-----ELVRRPERS----- 1505
Qy 977 VQIRDLS--GDAEADTISLDISEVDPAYLNLSDYDIKYLPEFPMIFRKVPKSAQPEPP 1034
Db 1506 -SVQDLRAVGEPLVRLSLSLSQ-----RLARTPPAQR----- 1538
Qy 1035 SPMAEEELAEFPETWPMGELGPHAGLETTESSEVDALLABAAVGRKEKW----- 1086
Db 1539 -----HPANARGDG-----ESSEGSARGSPVLAVRRRLSFLERLS 1578
Qy 1087 -----SSFSRLHFPGRHLLPDEPAELGRERVKASVEHIGRIKGRP----- 1130
Db 1579 SRLQSGSSEDSGASGRSTPL-----FGLRRATSEGESLRL--GLPHNQLAAQAGAT 1631
Qy 1131 -----EGLEKEGP-----PRKKPGLASFLSG-----LK 1154
Db 1632 TPSAESLGSEASATSGSAPGESRSLRWGFSRPRKDKGLSPNLASVQEBLGHQVYRS 1691
Qy 1155 SWDRAPPTLRELSDETIVLQSVTLACQVSAQAQAATWSKOGAPLESRRVLISATLKN 1214
Db 1692 ESDFPFVPHIKLKDQVLEGEAATLLCLPAACAPAPIHSMKKDKSLRSEPSVIVISCKDG 1751
Qy 1215 FQLLTILVVAEDLGVTCTSVNALGVTVTGVLKRAERPSSPCPDIGEVADGVLLVW 1274
Db 1752 RQLLSIPRAGKRAHAGLCCATVNLGSIITSSCTVAVARVPGKLAPPEVPTQDTALVLM 1811
Qy 1275 KPVESYGVNTIVOCLESLEGS--WTTLASDIFDCCYLTSKLSRGCTTFTTACVSTAGMGP 1333

Db 1812 KPGRSAPCTYTLERRVDGESVMHPVSSGIPDCYYNVNTHLPVGVTVPFRVACANRAGQGP 1871
Qy 1334 YSSPSQVLLGG----- 1345
Db 1872 FSNSEKVFVRGTQDSSAVPSAAHQEAQVTSRPARARPPDSDTSLAPPLAPAPTFFPSVT 1931
Qy 1346 -----PSHLASEESQ-----RSAQP-LPST----- 1366
Db 1932 VSPSSPTTPSQALSSLKAVGPPQTPRRHRGLQAARPAEPTLSTHTVTFSEPKPFVLD 1991
Qy 1367 ----- 1366
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Qy 1367 -----KTFAPQTOIORGRFSVVQRQCKWAKASGRALAALPIIP 1401
Db 2052 VSSFGSPSSRSPRECTTLRQGPQPKPTFLFEKARGFVVRACRENATGTFVAKIVP 2111
Qy 1402 YHPKDTAVLREYEA-LGLRHPLHAQLHAAVLSPRHLVLIILELCSGPPELLPCLAEASYS 1461
Db 2112 YAAEGKRVLQIEYEVLRTLHHEEIMSLHEAYITPYLVLLAESCGNRELLCGLSDRFRYS 2171
Qy 1462 ESBVKDYLWQMSATQYLHNLHILHLDURSENITEYNLLKVDLGNQASLSQSKVLPS 1521
Db 2172 EDDVATYVQLLQGLDYLGHVHLHDIKPDNLLAPDNALKIVDFGSAQFYNQALRPL 2231
Qy 1522 DKPKDYLETWAPLELGGGAVPQTDIWAIGTAFIMLSAEYFVSSEGARDLQRLKGLV 1581
Db 2232 GHRTGTLEFNAPEWYKGEPIGSATDIWAGVLYTILMSGRSPFYEPDQETEARIVGSRF 2291
Qy 1582 RLSCRYAGLSGGNAVFLRSTLCAQWGRPCASSCLOCPLWTEEGPACSRPAPVTFPTARL 1641
Db 2292 DAFQLYPNTSQSATFLRKVLSVHPMSRPSLODCLAHPWLODAYLMKLRRLTFTTTNRL 2351
Qy 1642 RVFVRNREKRRALLYKRNHL 1661
Db 2352 KEFLGQRRERAEATRHKV 2371
RESULT 15
ADE47676
ID ADE47676 standard; protein; 3208 AA.
XX AC ADE47676;
XX DT 29-JAN-2004 (first entry)
XX DE Human NOV14c protein SEQ ID NO:38.
XX KW human; cardiant; antiarteriosclerotic; hypotensive; immunosuppressive;
KW dermatological; anorectic; cytostatic; antidiabetic; haemostatic;
KW anti-HIV; antiasthmatic; antibacterial; virucide; neuroprotective;
KW neotropic; antiparkinsonian; antilipaemic; gene therapy; vaccine.
XX OS Homo sapiens.
XX WO2003076642-A2.
XX PN 18-SEP-2003.
XX PD 02-AUG-2002; 2002WO-US024459.
XX PF 02-AUG-2001; 2001US-0309501P.
XX PR 03-AUG-2001; 2001US-0310291P.
XX PR 08-AUG-2001; 2001US-0310951P.
XX PR 09-AUG-2001; 2001US-0311292P.
XX PR 13-AUG-2001; 2001US-0311979P.
XX PR 14-AUG-2001; 2001US-0312203P.
XX PR 17-AUG-2001; 2001US-0313156P.
XX PR 17-AUG-2001; 2001US-0313201P.
XX PR 20-AUG-2001; 2001US-0313702P.
XX PR 21-AUG-2001; 2001US-0314031P.
XX PR 23-AUG-2001; 2001US-0314466P.

PR 28-AUG-2001; 2001US-0315403P.
PR 29-AUG-2001; 2001US-0315853P.
PR 31-AUG-2001; 2001US-0315808P.
PR 21-SEP-2001; 2001US-0323936P.
PR 03-DEC-2001; 2001US-0338078P.
PR 05-FEB-2002; 2002US-0354555P.
PR 05-MAR-2002; 2002US-0361764P.
PR 13-APR-2002; 2002US-0373825P.
PR 15-MAY-2002; 2002US-0380971P.
PR 16-MAY-2002; 2002US-0380980P.
PR 28-MAY-2002; 2002US-0383761P.
PR 29-MAY-2002; 2002US-0383887P.
PR 01-AUG-2002; 2002US-00210130.
XX (CURA-) CURAGEN CORP.
XX
XX Zernhusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;
PI Pena CEA, Shinkens RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;
PI Boldog FI, Padigaru M, Smithson G, Shenoy SG, Ji W, Gorman L;
PI Verdet CAM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;
PI Burgess CE, Khramtsov NV, Ort T, Ellerman K, Rastelli L, Agee M;
PI Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eileen A, Gangolli EA;
PI Giot L, Ooi CS, Rothenberg ME, Spaderna SK, Hjalt T, Liu X;
PI Taupier RJ, Catterton E;
XX
XX WPI; 2003-779062/73.
DR N-PSDB; ADE47675.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes,
PT atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
PT or pharmacogenomics.
XX
XX Claim 1; SEQ ID NO 38; 562pp; English.
XX
XX The invention relates to a novel (NOVX) human polypeptide. A polypeptide
CC of the invention has cardiac, antiarteriosclerotic, hypotensive,
CC immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,
CC haemostatic, anti-HIV, antitubercular, antibacterial, virocidic,
CC neuroprotective, neurotropic, antiparkinsonian, and antilipidemic activity.
CC A polynucleotide encoding a polypeptide of the invention may have a use
CC in gene therapy, and as a vaccine. A polypeptide of the invention is
CC useful in the manufacture of a medicament for treating a syndrome
CC associated with a human disease, the disease selected from a pathology
CC associated with the polypeptide. These may also be used in diagnosis,
CC treating or preventing NOVX-associated disorders such as cardiomyopathy,
CC atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
CC haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,
CC multiple sclerosis, infections, anorexia, cancer-associated cachexia,
CC neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's
CC disease), haematopoietic disorders, dyslipidaemias and other wasting
CC disorders associated with chronic diseases. The nucleic acids are also
CC used as hybridisation probes, in chromosome mapping, tissue typing,
CC preventive medicine, and pharmacogenomics. The polypeptides are also
CC useful as vaccines. The present sequence represents a NOVX polypeptide of
CC the invention.
XX
SQ Sequence 3208 AA;
Query Match 22.6%; Score 1973; DB 7; Length 3208;
Best Local Similarity 29.3%; Pred No. 8, 6e-115;
Matches 568; Conservative 236; Mismatches 639; Indels 498; Gaps 50;
QY 54 PSNQVITRDVQAGTGTQAFEMIEGDPQPSVYWKQSVQLVDSRSLSQOQGGTTLSVL 113
DB 1426 PRFESIMEVGVGAGETARFAVVGKFLPDIMYKQEVLLTSSSHVSFVYNECSLV 1485
QY 114 RHVASKDAGVYVYCLAQNTGGQVLCRAELLVLGGDN---EPDSKQSHR-RKLHSFYEVK 168
DB 1486 LSTGAQDGGVYVYCTAQNLAGVSCAKELAVHSAQTAMEVGVGDEDEHGRRLSDFDIH 1545
QY 169 BEIGHGVFVVRVQKGNKILCAKPIPLSRTRTAQYRERDILALSHPLVTGLLDQF 228

DB 1546 QEIGRGAFSYLRRIVERSSGLEFAAKFTPSQAKPKASARRRLLARLHDCVLYFHEAF 1605
QY 229 ETRKTLIILILCSSEELLRLYKGVVTEAEVKVYIQQOLVEGLHYLHSHGVLDLKPS 288
DB 1606 ERRRLVIVTELCTEELLERIAKFTVCESEIRAYMRQVLEGIHYLHSHGVLDLKPS 1664
QY 289 NILMVHPA--REDIKICDFGAQITFAELQFSGSPFVSPFIIQQNPVSEASDIWAM 346
DB 1665 NLLVWDGAAGQOVKRICDFGNAQLTGPQYQCYGTPEFVAPFVNVQSPVSGVTDIWPV 1724
QY 347 GVISYLSLTCSPFAGSDRATLNVLEGRVSWSPMAHLSEDAKDF-1KATLQAPQA 405
DB 1725 GVVAFCLTGTSPFVGENDRTLMNINNVNVAPEFTFLSLRREARGLIKVLVQ--DRL 1782
QY 406 RPSAAQCLSHPWFLKSMPEAEAHFINTKQLFLARSQRWQSLMSYKSLIMKRSIPPELLR 465
DB 1783 RPTASEETLEHFWFKTQAKGAE---VSTDHLKLFLSRWRQSRQISYKCHLVLPPELLR 1839
QY 466 GPDPSPSLGVARHLCDRGGSSSSSSSSDNEL-----APRAAK-SLPPSPVTH 513
DB 1840 APPERVWVTPRR-PPSGGSSSSSDEEELPSVPLQPEFGSGRSLVTDITED 1898
QY 514 SPLHPRGFLRPSASLPPEAEASERSTEAPAPPASPEGAGPPAAQGCVPVRHSVIR----- 568
DB 1899 BALGTFTGAATPMQWQEQGFAPSDQEQAPSPALPSFGQEPAA-GASPRGELRGCSSA 1957
QY 569 -----SLFYHQAG--ESPFGALAPG-----SRHPARRRHLK 600
DB 1958 ESALPRAGPRELGLHKAASVELPQRSPGPGNATRLARGLGEYGAQLQRLQRLR 2017
QY 601 GGYIAGALPGLREPLMEH-----RVLEEAAREEQATL-----LAKAFSFTALR 645
DB 2018 GGPEDGVSLGLRPLLESGLGRARDPRMAAASSEAAPHQPPLENRGLQKSSFSQCEA 2077
QY 646 LPASOTHLAPGHSHLEHDSPTPR-----PSSACGAQRLPSAPSGGAFIRDMGHPOGS 701
DB 2078 EP-RGRHRRAGAPLEI PVARLGARLQESLSALSEAQ--PSPA-----RPSAP 2125
QY 702 KQLPSTGHTGHTAQPERSPDPMWGQAPFCHPXQSGAPQEGGSPHAPVACPFPGFPFG 761
DB 2126 K--PST---PKSARFSAITPSPADPQPAP--QPAQDKAPRPFPRVRAKAPAP---PPQ 2174
QY 762 SCK--EAPLVSPSSFLQ-----POAPAPAK-----ASPPLDSKMG 797
DB 2175 ALQTLAULTYAGIILQSLQSGHAQSPGPAAPSEPKFAHAFARVASPP----- 2227
QY 798 GDISLPGRPKPGPCSPGASQASSQVSSLRVGSSQVGTGPGPSLDAGWTQAEADLSD 857
DB 2228 -----PCAPEKRVPSAGGPPVLAFAKARVPT-----VPPRPGSSLSSTIENTLESAVPE 2275
QY 858 STPTLQRPQEQVTRKFTSLGRCGYAGVAGYGTFAFGDAGGMLQGPMMWARIAMAVSOS 917
DB 2276 A--XFKRSRES-----PLSLGLR-----LLSR 2296
QY 918 EEEQOEAR-ABSQSEQQARAEPLPQVSAAPVGVGRAPTRSPPEPTPWEDICQVSL 976
DB 2297 RSEERGPFPGABEEDGIYRFPSPAGTPL-----ELVRRPERSR----- 2333
QY 977 VQIRDLG--GDAAADTISLDIGEDVAYLNLSDLYDIKYLPEFMIFRKVPKSAQPEP 1034
DB 2334 -SVQDLRAVGEPGLVRLSLSLSQ-----RLRTPPAQR----- 2366
QY 1035 SFMAEELAEFPETPTWPGELGPHAGLETESDNDALLAAVGRKRW----- 1086
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QY 1131 -----EGLEKEGP-----PRKPGLASPRLSG-----LK 1154

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QY 1155 SWDRAPFLRELSDETIVLQSVTLACQVSAQPAQAATWSKDGAPLESSESRVLISATLKN 1214
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QY 1215 POLITILVVAEDIGVYTCVSNALGVTITGTVLRKAERPSSSPCPDIGEVYADGVLLVW 1274
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QY 1275 KPVSYSYGPVTYIVQCSLEGGG-WTTLASDIPDCCLYLSKLSRGCTYTFRTACVSKAGMP 1333
Db 2640 KPGDSRAPCTYTLERRVDGESVWHPVSSGIPDCYVNVTHLPVGVTVRFRVACANRAGOGP 2699
QY 1334 YSSPSEQVLLGG----- 1345
Db 2700 FSNSEKVFVGTQOSSAVPSAAHQEAFTVSRPARARPPDSPTSLAPLAPAAFTPPSVT 2759
QY 1346 -----PSHLASEESOG-----RSAQP-LPST----- 1366
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QY 1367 ----- 1366
Db 2820 TGTPIPASTPQGVKVPVSSSTPVVVVTSFVSAPPAPPEPPPEPTKVTVQSLSPAKEY 2879
QY 1367 -----KTEAFOTQIORGRFSVVROCKEKASGRALAAKIIP 1401
Db 2880 VSSPGSSPRSPREGITLROGPQKPYTFLEEKARGFGVVRACRENATGRTFVAKIVP 2939
QY 1402 YHPKDKTAVLREYEALKGLRHPHLAQLHAAYLSRHLVLIILELCSGPPELLPCLAEASYS 1461
Db 2940 YAAEKKRRVLQEVYVRLTHERIMSLHEAVITPRYLVIAESCGNRELLCGLSDRFRYS 2999
QY 1462 ESEVKDYLWQMLSATQYILHNOHIIHLDLRSENMIITEYNLLKVYDLGNAQSLSOEKVLP 1521
Db 3000 EDDVATYVQLLQGS-DYLLGHGHVHLHLDIKPNLLAPDNALKIVDFGSAQFYNPQALRPL 3059
QY 1522 DKFKDYLETMAPELLEGGGAVPQIDWAIQVTAFTIMLSAEBYFVSSEGARDLQGLRKLGV 1581
Db 3060 GHRTCTLEFMAPENVKGPISATDINGAGVLTIVILSGRSFVEYPPDQETEARIVGGRF 3119
QY 1582 RLSRCYAGLSGGAVAFIRSTLCAOPWGRPCASSCLQCPWLTEEGPACSRPAPVTFPTARL 1641
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QY 1642 RVFVNRKRRALLYKRHL 1661
Db 3180 KEFLGEQRRRAAATRHKV 3199

Search completed: April 23, 2004, 15:09:09
Job time : 93 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:07:27 ; Search time 30 Seconds
(without alignments)
2865.241 Million cell updates/sec

Title: US-10-697-263-2

Perfect score: 8740

Sequence: 1 MGCCRLGCGGCSVAHSVSG.....RNREKRALYKRNHQAQR 1665

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pdp.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pdp.*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8740	100.0	1665	4	US-09-858-664A-2
2	8740	100.0	1665	4	US-10-274-978-2
3	1173	13.4	846	4	US-09-858-664A-3
4	1173	13.4	846	4	US-10-274-978-4
5	893	10.2	549	4	US-09-858-664A-5
6	893	10.2	549	4	US-10-274-978-6
7	592.5	6.8	414	4	US-09-858-664A-13
8	592.5	6.8	414	4	US-10-274-978-14
9	591.5	6.8	2860	2	US-08-826-267-2
10	531	6.1	279	4	US-09-858-664A-4
11	531	6.1	279	4	US-10-274-978-5
12	521	6.0	298	4	US-09-858-664A-17
13	521	6.0	298	4	US-10-274-978-18
14	509.5	5.8	508	4	US-09-858-664A-18
15	509.5	5.8	508	4	US-10-274-978-19
16	504	5.8	260	4	US-09-858-664A-6
17	504	5.8	230	4	US-10-274-978-7
18	489	5.6	448	2	US-09-159-385-2
19	489	5.6	448	3	US-09-186-277-2
20	472.5	5.4	260	2	US-07-857-224B-23
21	466.5	5.3	454	2	US-09-159-385-1
22	466.5	5.3	454	3	US-09-186-277-1
23	466	5.3	274	4	US-09-858-664A-14
24	466	5.3	274	4	US-10-274-978-15
25	465	5.3	358	4	US-09-230-896C-29
26	463.5	5.3	1050	4	US-09-428-711A-16
27	456	5.2	331	3	US-08-810-712-24

ALIGNMENTS

RESULT 1

US-09-858-664A-2

; Sequence 2, Application: US/09858664A

; Patent No. 6482624

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui, et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL000927-CIP

; CURRENT APPLICATION NUMBER: US/09/858,664A

; PRIORITY FILING DATE: 2001-05-17

; PRIOR APPLICATION NUMBER: 09/711,134

; PRIORITY FILING DATE: 2000-11-11

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1665

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-858-664A-2

Query Match		100.0%;	Score 8740;	DB 4;	Length 1665;
Best Local Similarity		100.0%;	Pred. No. 0;		
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				Indels	0;
				Gaps	0;
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DB	1	MGCCRLGCGGCSVAHSVSGGLTNHPSVMYCGWHFPLCGWGGGLHSSLPALPGPPSMQVTI	60		
QY	61	EDVQACTGTAQFEAIIIEGDPQPSVWYKDSVQLVDSVTRLSQQQEGTYSLVLRHVASKD	120		
DB	61	EDVQACTGTAQFEAIIIEGDPQPSVWYKDSVQLVDSVTRLSQQQEGTYSLVLRHVASKD	120		
QY	121	AGVYTCIAQNTGGVLCXAELLVGGNEPDSEKSHRKLHSHFYKVEIGRGVGFVK	180		
DB	121	AGVYTCIAQNTGGVLCXAELLVGGNEPDSEKSHRKLHSHFYKVEIGRGVGFVK	180		
QY	181	RVQHGKNIKLAAPFIPURSTRQAQYRERDILAAASHPLVTGLDQFETRKTLILLEL	240		
DB	181	RVQHGKNIKLAAPFIPURSTRQAQYRERDILAAASHPLVTGLDQFETRKTLILLEL	240		
QY	241	CSSEELLRLYKRGVVTAEAEVKYIQQLVEGLHYHSHGVHLHDIKPSNLMVHPAREDI	300		
DB	241	CSSEELLRLYKRGVVTAEAEVKYIQQLVEGLHYHSHGVHLHDIKPSNLMVHPAREDI	300		
QY	301	KICDFGAQNTTRAELOFQSGSPFVSPEIIQONPVSEASDIWAMGVISYLSLTCSPP	360		
DB	301	KICDFGAQNTTRAELOFQSGSPFVSPEIIQONPVSEASDIWAMGVISYLSLTCSPP	360		

Sequence 10, Appl
Sequence 4, Appl
Sequence 14, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 22, Appl
Sequence 5, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 31, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 24, Appl
Sequence 34, Appl
Sequence 32, Appl

361	QY	AGESDRA	TLLNV	LG	RVSWS	SP	WAAHL	SED	KD	F	I	KATL	Q	R	A	P	O	A	P	S	A	A	C	L	S	H	P	W	F	L	K	420																							
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421	QY	SMPAE	EAHF	I	N	T	K	L	L	A	R	S	R	W	O	R	S	L	M	S	K	I	L	W	R	S	I	P	E	L	L	R	G	P	D	S	I	G	V	A	R	H	L	C	480										
421	Db	SMPAE	EAHF	I	N	T	K	L	L	A	R	S	R	W	O	R	S	L	M	S	K	I	L	W	R	S	I	P	E	L	L	R	G	P	D	S	I	G	V	A	R	H	L	C	480										
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541	Db	EAPAPP	AS	PEG	A	Q	P	P	A	A	G	G	V	P	A	R	H	S	I	R	S	I	L	F	Y	H	Q	A	G	E	S	P	E	H	G	A	L	A	P	G	S	R	R	R	P	A	R	R	L	L	K	600			
601	QY	G	G	Y	A	N	A	L	P	C	L	P	E	M	E	H	R	V	L	E	E	A	R	E	O	A	T	L	L	A	K	A	P	S	F	E	T	A	L	L	P	A	S	G	T	H	L	A	P	G	H	S	660		
601	Db	G	G	Y	A	N	A	L	P	C	L	P	E	M	E	H	R	V	L	E	E	A	R	E	O	A	T	L	L	A	K	A	P	S	F	E	T	A	L	L	P	A	S	G	T	H	L	A	P	G	H	S	660		
661	QY	LEHDS	P	S	T	P	R	S	S	E	A	C	G	E	A	Q	R	L	P	S	A	P	G	G	A	P	I	R	D	M	G	H	P	Q	G	S	K	O	L	P	S	T	G	H	E	P	T	A	P	R	P	S	720		
661	Db	LEHDS	P	S	T	P	R	S	S	E	A	C	G	E	A	Q	R	L	P	S	A	P	G	G	A	P	I	R	D	M	G	H	P	Q	G	S	K	O	L	P	S	T	G	H	E	P	T	A	P	R	P	S	720		
721	QY	PDS	P	M	G	O	A	P	C	H	E	K	O	S	A	P	O	E	C	S	D	H	P	A	V	A	C	P	G	S	P	P	G	S	C	K	E	A	P	L	P	S	S	P	L	G	O	P	A	780					
721	Db	PDS	P	M	G	O	A	P	C	H	E	K	O	S	A	P	O	E	C	S	D	H	P	A	V	A	C	P	G	S	P	P	G	S	C	K	E	A	P	L	P	S	S	P	L	G	O	P	A	780					
781	QY	P	P	A	K	A	S	P	P	L	D	S	K	M	G	P	E	D	-	S	L	P	R	K	P	G	P	C	S	S	P	S	A	S	C	A	S	S	S	Q	V	S	S	L	R	V	G	S	O	V	T	E	P	G	840
781	Db	P	P	A	K	A	S	P	P	L	D	S	K	M	G	P	E	D	-	S	L	P	R	K	P</																														

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1441 ILELCSGPPELLCLAEAGSYSESVKDYLNQWMLSATQYLHNOHILHLDLRSENMIIETYN 1500
1501 LLKVVDLGNAQSLSOBKVLPSDKFYLETMAPELLEGCGAVPQTDIWAIGVTAFTMLSA 1560
1501 LLKVVDLGNAQSLSQEKVLPSDKFYLETMAPELLEGCGAVPQTDIWAIGVTAFTMLSA 1560
1561 EYVSVSEGGARDLQGRKGLVRLSRCYAGLSGGAFAFLSTICAQPWGRPCASSCLQCPW 1620
1561 EYVSVSEGGARDLQGRKGLVRLSRCYAGLSGGAFAFLSTICAQPWGRPCASSCLQCPW 1620
1621 LTEEGPACSRPAPVTFPTTARLRFVFNREKRRLALYKRNHLAQVR 1665
1621 LTEEGPACSRPAPVTFPTTARLRFVFNREKRRLALYKRNHLAQVR 1665

RESULT 2
US-10-274-978-2
; Sequence 2, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1665
; TYPE: PRT
; ORGANISM: Human
US-10-274-978-2

Query Match 100.0%; Score 8740; DB 4; Length 1665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1	MGCCRLCGCGCSVAHVSVOGLTNHPSVMWCGHPGLCGWGGGLHSLPALPGPSPMQVTI	60
Db	1	MGCCRLCGCGCSVAHVSVOGLTNHPSVMWCGHPGLCGWGGGLHSLPALPGPSPMQVTI	60
QY	61	EDVQAQTGTAQFEALIEGDPOPSVTWYKDSQVLVDSTRLSQOQGGTTYSLVLRHVASXD	120
Db	61	EDVQAQTGTAQFEALIEGDPOPSVTWYKDSQVLVDSTRLSQOQGGTTYSLVLRHVASXD	120
QY	121	AGVYTCLAQNTGGQVLCKAELLVLGDNEPDSEKSHRRKLSHYEVKEEIEGRGVFGFYK	180
Db	121	AGVYTCLAQNTGGQVLCKAELLVLGDNEPDSEKSHRRKLSHYEVKEEIEGRGVFGFYK	180
QY	181	RVQHKGNKILCAAKFIPJRSRTRAQAYRERDILAALSHPLVTGLLDQPFTRKTLILLEL	240
Db	181	RVQHKGNKILCAAKFIPJRSRTRAQAYRERDILAALSHPLVTGLLDQPFTRKTLILLEL	240
QY	241	CSSEELLDLRYKGVVTVAEVKVYIQQLVEGLHYLHSHGVLEHLDIKPSNILMVHPAREDI	300
Db	241	CSSEELLDLRYKGVVTVAEVKVYIQQLVEGLHYLHSHGVLEHLDIKPSNILMVHPAREDI	300
QY	301	KICDFGAQNTIPAELOFSGPSPEFVGPEIIQQNPVSEASDIWANGVTSYLSLTCSSPFF	360
Db	301	KICDFGAQNTIPAELOFSGPSPEFVGPEIIQQNPVSEASDIWANGVTSYLSLTCSSPFF	360
QY	361	AGESORATILNVLEGVSWSSPMAHLSEDAKDFIKATLQRAQARPSAAQCLSHPWFLUK	420
Db	361	AGESORATILNVLEGVSWSSPMAHLSEDAKDFIKATLQRAQARPSAAQCLSHPWFLUK	420
QY	421	SMPAEAEHPINTKQLKFLIARGRWORSLMSYKSIILVMRSIPELLRGPPDPSGLGVARHLC	480

Db 421 SYPAEAEHFINTKQLKELLARSQRSLMSYKSLVWRSIFELLRGPDPSPSLGVAEHL 480
Qy 481 RDTGSSSSSSSSNEIAPFAKSLPSPVTHSFLHPRGFLRPSASLPEEAEASERST 540
Db 481 RDTGSSSSSSSSNEIAPFAKSLPSPVTHSFLHPRGFLRPSASLPEEAEASERST 540
Qy 541 EAPAPPASPEGAGPPAAQCGVPRHSVIRSLFYHQAGESPHEGALAPGSRHRPARRHLK 600
Db 541 EAPAPPASPEGAGPPAAQCGVPRHSVIRSLFYHQAGESPHEGALAPGSRHRPARRHLK 600
Qy 601 GGYIAGALPGLREPLMEHRVLEEEAAEEQATLLAKAPSPETALRLPASGTHLAPGHS 660
Db 601 GGYIAGALPGLREPLMEHRVLEEEAAEEQATLLAKAPSPETALRLPASGTHLAPGHS 660
Qy 661 LEHDSPTSPRESSACCEAOLPAPAGGABIRDMGHPQSGKOLPSTGGHPGTAQPERPS 720
Db 661 LEHDSPTSPRESSACCEAOLPAPAGGABIRDMGHPQSGKOLPSTGGHPGTAQPERPS 720
Qy 721 PDSWGOAPFCHPKQSGAPQEGSPHAPVPCPPGSPGSCKEAPLVPSPPFLGQPOA 780
Db 721 PDSWGOAPFCHPKQSGAPQEGSPHAPVPCPPGSPGSCKEAPLVPSPPFLGQPOA 780
Qy 781 PPAPAKASPPIDSKMGPDIDSLPGRPKPGCSSPGSASQASSQVSSLRVSSQVGTPEG 840
Db 781 PPAPAKASPPIDSKMGPDIDSLPGRPKPGCSSPGSASQASSQVSSLRVSSQVGTPEG 840
Qy 841 PSLDAGHTQBAEDLSSTPTLQRPQEQVTRKFSLGGRGGYAGVAGYGFAPFGDAGG 900
Db 841 PSLDAGHTQBAEDLSSTPTLQRPQEQVTRKFSLGGRGGYAGVAGYGFAPFGDAGG 900
Qy 901 LQCGPMWARIWAVSQSEEEQEARAESQSEEQEARAESPLPQVSAARPVEVGRAPTR 960
Db 901 LQCGPMWARIWAVSQSEEEQEARAESQSEEQEARAESPLPQVSAARPVEVGRAPTR 960
Qy 961 SSPPTPVEDIGVSLVOIRDLSGDAEAADTISLDISEVDPAVNLSDLDYDKLPEEFM 1020
Db 961 SSPPTPVEDIGVSLVOIRDLSGDAEAADTISLDISEVDPAVNLSDLDYDKLPEEFM 1020
Qy 1021 IPRKVPKSAQPPSPMAEELAEPEPTWMPGELPHAGLEITERSESDVALLAAAV 1080
Db 1021 IPRKVPKSAQPPSPMAEELAEPEPTWMPGELPHAGLEITERSESDVALLAAAV 1080
Qy 1081 GRKRWSSPSLSLPHFGRHPLDPEALGLRERVKASVEHISILKRPGLKEGPPR 1140
Db 1081 GRKRWSSPSLSLPHFGRHPLDPEALGLRERVKASVEHISILKRPGLKEGPPR 1140
Qy 1141 KXPGLASFLSLGKSWDRAPTLRELSDETIVVVGOSVTLACQVSAQAAQATWSKDAPL 1200
Db 1141 KXPGLASFLSLGKSWDRAPTLRELSDETIVVVGOSVTLACQVSAQAAQATWSKDAPL 1200
Qy 1201 ESSRVLISATIKNFQLTILVVAEDIGVYTCVSNALGVTITVGLRKAEPSSSPCP 1260
Db 1201 ESSRVLISATIKNFQLTILVVAEDIGVYTCVSNALGVTITVGLRKAEPSSSPCP 1260
Qy 1261 DIGEVVADGVLLVWKPVSYPVTYIVQCSLEGGSWTTLASDIFDCCYLTSKLSRGTYT 1320
Db 1261 DIGEVVADGVLLVWKPVSYPVTYIVQCSLEGGSWTTLASDIFDCCYLTSKLSRGTYT 1320
Qy 1321 FRTACVSKAGMGFSPSEQVLLGQPSHLASBEESQGRSAQPLPSTKTFAPQTOIGRPF 1380
Db 1321 FRTACVSKAGMGFSPSEQVLLGQPSHLASBEESQGRSAQPLPSTKTFAPQTOIGRPF 1380
Qy 1381 SVVROCKEASGRALAAKIIIPYHKDKTAVLREYALKGLRHPHQAOLHAAYLSPRHVL 1440
Db 1381 SVVROCKEASGRALAAKIIIPYHKDKTAVLREYALKGLRHPHQAOLHAAYLSPRHVL 1440
Qy 1441 ILELCGPELLPCLABRASYSSEVKDYLWQMLSATQYLNHQLHLDRSENMIITEYN 1500
Db 1441 ILELCGPELLPCLABRASYSSEVKDYLWQMLSATQYLNHQLHLDRSENMIITEYN 1500
Qy 1501 LLKXVDLGNASQSLQSKVLPSDKFDYLETMAPELLEGQAVPQTDIWAIGVTAFLMSA 1560

Db 1501 LLKXVDLGNASQSLQSKVLPSDKFDYLETMAPELLEGQAVPQTDIWAIGVTAFLMSA 1560
Qy 1561 EYPVSEGNARDLQGRKGLVRLSCYAGLSGGAVALRSTLCAQFWGPRPCASSCLQCPW 1620
Db 1561 EYPVSEGNARDLQGRKGLVRLSCYAGLSGGAVALRSTLCAQFWGPRPCASSCLQCPW 1620
Qy 1621 LTEEGPACSRPAPVTFTPTARLVFVVRNEKRRALLYKRNHLAQVR 1665
Db 1621 LTEEGPACSRPAPVTFTPTARLVFVVRNEKRRALLYKRNHLAQVR 1665
RESULT 3
US-09-858-664A-3
; Sequence 3, Application US/09858664A
; Patent No. 6482624
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-3
Query Match 13.4%; Score 1173; DB 4; Length 846;
Best Local Similarity 34.9%; Pred. No. 5.7e-62;
Matches 313; Conservative 121; Mismatches 316; Indels 146; Gaps 29;
Qy 54 PSMQVTEVDQAQTGTAQFAEAIIEGDPQPSVTWYKDSVQLVDSTRLSQOQEGTTVSLV 113
Db 1 PRFESIMEDVEVGAGETARFAVVVEGKPLDIDMWYKDEVLLTSSHSVFWYENECSLV 60
Qy 114 RHVASDKAGVYTCLAQNTGQVLCRAELVLVLDGN---EPDSEKQSHR-RKLHSEVEVK 168
Db 61 LSTGAQDGGVYTCTAQNLAGVSCAEALVHSAQTAAMEVEGVEDDHRRRLUSDYDILH 120
Qy 169 EETGRGVFGVFRVQKNGKILCAAKFIPLRSTRQAAYRERDILAAALSHPLVTGLDQF 228
Db 121 QETGRGAFSLRIVERSSGLEFAAKFIPSAKPKASARREARLLARLQHCVLVPEAF 180
Qy 229 ETKTILILELCSSBEELDLRYKGVVTEAEVKVIQOLVEGLVHLHSHGVHLHDIKPS 288
Db 181 ERRRGLVITELC-TEELLERIAKPTVCESTRAYMRQVLEGVHSHVHLHDVKPE 239
Qy 289 NILMVHPA--REDIKICDFGAQNTIPELQPSQVSGPFEVSPETIIQQNPVSEASDIWAM 346
Db 240 NLVWDGAGQGVRCDFGNAQELTPGEPQCOYGTPEFAPEIVNQSPVSGVTDIWPV 299
Qy 347 GVTSYLSLTCSSPFAGESDRATLLNVLGRVSWSSPMAHLSEDADKF-IKATLQAPQA 405
Db 300 GVAFLCLTAGISPFVGENDRRTLLMNIRNVNVAPEETTFLSLREARGFLIKVLVQ--DRL 357
Qy 406 RPSAAQCLSHPLWPKMPAEAEHFNKQIKFLARSWRQSIKSLVWRSIPPELLR 465
Db 358 RPTAEETLEHPNFKTQAKGAB---VSTDHLKFLSRRRWQRQSIYKCHLVLPPELLR 414
Qy 466 GPPDSPSLGVARHLCDTGGSSSSSSSSSSDNEL-----APFARAK-SLPPSPVTH 513
Db 415 APFVWVWTPRR-PPPSGGLSSSSSEEELEELPSVPRPLQPEFSGRSVSLTDIPTED 473
Qy 514 SPLHPRGFLRPSASLPEEAEASERSTEAPAPASPEGAGPPAAQCVPRHSVIR----- 568
Db 474 EALGTPTGAATPMQWQEQRAPSDQEPALPSQEPALPSQEPALPSQEPALPSQEPALPS 532

QY 569 -----SLFYHQAG--ESPHEGALAPG-----SRHPARRHLK 600
Db 533 ESALPRAGPRELGRGLHKAASVLPORRSGPGATRLARGGEGEYACQALQRLR 592
QY 601 GGYIAGALPGLRPLMEH-----RVLEEEAAREEQATL-----LAKAPSPETALR 645
Db 593 CGPEDGKVSGLRGLPGLLESIGGRARDPRMARAAASSEAAAPHQPPLENRGLQKSSSFSQGEA 652
QY 646 LPASGTHLAPGHSHLSHDSSTPR-----PSSEACGEAORLPSAPSGGAPIRDMGHPOGS 701
Db 653 EP-RGRHRRAGAPLETPVARLGARLQESPSLSALSEAQ--PSSPA-----RPSAP 700
QY 702 KQPLSTGGHGTGAQPERPSDPWQGPAPFCHPKQGSAPQEGSCSPHPAVAPCPGSPFP 761
Db 701 K--PST---PKSAEPSATTPSDAQPAP--QPAQDKAPEPRPEVRASKAP-----PPQ 749
QY 762 SCK--EAPLVPSPFFLQG-----POAPPAPAK-----ASPPLDSKMG 797
Db 750 ALQTLALPLTPYAIQIQLSGLSHAQPSQGPAAFPSEKPHAAVAVARVAPP-----802
QY 798 GDISLPGRPKPGPCSSPGSASQSSQVSLRVGSSQVTEPGPSLDAEGWQTQAB 853
Db 803 -----PGAPEKRVPSAGGPPVLAEKARVPT-----VPPRPGSSLSSENLESE 846

RESULT 4
US-10-274-978-4
; Sequence 4, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Human
US-10-274-978-4

Query Match 13.4%; Score 1173; DB 4; Length 846;
Best Local Similarity 34.9%; Pred. No. 5.7e-62;
Matches 313; Conservative 121; Mismatches 316; Indels 146; Gaps 29;

QY 54 PSMQVTEVQATGTAQTAQFAIIEGDPQPSVTWYKDSVOLVDSVTRLSQQQEGTYSVLV 113
Db 1 PPFESIMEDVEVGAGETARFAVVVEGKPLDMMYKDEVLTTESSHVSVFYNEECSLVV 60
QY 114 RHVASKDAGVYTCIAQNTGGQVLCKAELLVLGGDN---EPDSEKQSHR-RKLHSFYEVK 168
Db 61 LSTGAQGGVYTCIAQNLAGEVSCKALAVSHAQTAAMEVGEVGEDEHGRRLSDFFDIH 120
QY 169 EETGRGVGVKRVQKHGKILCAAKFPLRSTRTAQYRERDILAAHSHPLVTLGLDQF 228
Db 121 QETGRGAFSVLRIVERSSGLSFAAKFIPSOAKPKASARREARLLARLQHDVLYFHEAF 180
QY 229 ETRKTLILILELCSSELDRLRYKGVVTEAVKVVIQOLVEGLHLSHGVLDLIDKPS 288
Db 181 ERRGLVIVTELC-TSELLERARKPTVCEIRAYMQVLEGIHYLHQSHVHLVDKPE 239
QY 289 NILMTWPA--REDIKCDGFGAQTTPAELQFSQSGSPFVSPEIQQNVFSEASDIWAM 346
Db 240 NLLVMDGAAGEQVRCDFNAQELTPGEPQCYQGTPEFAPEIVNQSPVSGVTDIWPV 299

QY 347 GVISVLSLTCSPFFAGESDRATLLNVLEGRVSWSPMAHLSEDAKOP-IKATIQAPQA 405
Db 300 GVVAFLCLTGISFFVGENDRITLMNRYNVAFBETTFSLSRREARGFLIKVLVQ--DRL 357
QY 406 RPSAAQCLSHPWFLKMPAEAAHFINTKQLXFLARSQWQSLMSYKSLVMRSTPELLR 465
Db 358 RPTAETLEHPWFKTKQAGAE---VSTDHLKFLSRRWQSQSYKCHLVLRIPPELLR 414
QY 466 GPDPSPSLGVARHLCDTGGSSSSSSSDNEL-----APFAK--SLPSPSVTH 513
Db 415 APPERVWVMPRR-PPPGGLSSSSDSEEELELPSVPRPLQEPFSGSVSLTDITD 473
QY 514 SPILLHPRGFLRPSASLPSAEASERSTAPAPSPAGAPPAAGCGVPRHSVIR-----568
Db 474 EALGTPTGAATMDWQOGRAPSDQAPSPFEALPSPGQEPAA-GASPRRGERLGRSSA 532
QY 569 -----SLFYHQAG--ESPHEGALAPG-----SRHPARRHLK 600
Db 533 ESALPRAGPRELGRGLHKAASVLPORRSGPGATRLARGGEGEYACQALQRLR 592
QY 601 GGYIAGALPGLRPLMEH-----RVLEEEAAREEQATL-----LAKAPSPETALR 645
Db 593 CGPEDGKVSGLRGLPGLLESIGGRARDPRMARAAASSEAAAPHQPPLENRGLQKSSSFSQGEA 652
QY 646 LPASGTHLAPGHSHLSHDSSTPR-----PSSEACGEAORLPSAPSGGAPIRDMGHPOGS 701
Db 653 EP-RGRHRRAGAPLEIPVARLGARLQESPSLSALSEAQ--PSSPA-----RPSAP 700
QY 702 KQPLSTGGHGTGAQPERPSDPWQGPAPFCHPKQGSAPQEGSCSPHPAVAPCPGSPFP 761
Db 701 K--PST---PKSAEPSATTPSDAQPAP--QPAQDKAPEPRPEVRASKAP-----PPQ 749
QY 762 SCK--EAPLVPSPFFLQG-----POAPPAPAK-----ASPPLDSKMG 797
Db 750 ALQTLALPLTPYAIQIQLSGLSHAQPSQGPAAFPSEKPHAAVAVARVAPP-----802
QY 798 GDISLPGRPKPGPCSSPGSASQSSQVSLRVGSSQVTEPGPSLDAEGWQTQAB 853
Db 803 -----PGAPEKRVPSAGGPPVLAEKARVPT-----VPPRPGSSLSSENLESE 846

RESULT 5
US-09-858-664A-5
; Sequence 5, Application US/09858664A
; Patent No. 6482624
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-5

Query Match 10.2%; Score 893; DB 4; Length 549;
Best Local Similarity 44.0%; Pred. No. 1.7e-45;
Matches 179; Conservative 79; Mismatches 135; Indels 14; Gaps 7;

QY 54 PSMQVTEVQATGTAQTAQFAIIEGDPQPSVTWYKDSVOLVDSVTRLSQQQEGTYSVLV 113
Db 147 PPFESIMEDVEVGAGETARFAVVVEGKPLDMMYKDEVLTTESSHVSVFYNEECSLVV 206
QY 114 RHVASKDAGVYTCIAQNTGGQVLCKAELLVLGGDN---EPDSEKQSHR-RKLHSFYEVK 168

Db 207 LSTGAQGGVYCTAQNLAGVSCAKELAVHSAQTAMEVEGVGEDHRRGLSDFYDIH 266
QY 169 BEIGRGVFGVKRVQHKGNKILCAKFIPLRSRTRACAVRERDILALSHPLVTGLDQF 228
Db 267 QEIGRGAFSYLRIVERSSGLEFAKFIPLSQAKPKASAREALLARLQHDVCVLYFHEAF 326
QY 229 ETRKTLILILELCSBELLDRLYKGVVTEAEVKVYIQQLVEGLYHSHGVHLHDIKPS 288
Db 327 ERRGLVITVELC-TEELLERIAKPTVCESEIRAYMRQVLEGIHYHSHVHLHDVKPE 385
QY 289 NILMVHPA--REDIKICDFGAQNTPAELQFSGYSGPSPFVSPETIIQQNPVSEASDIWAM 346
Db 386 NLLVWDGAGQVQVRIQDFGNAQELTGEPOYCYGTPTPEFAVEIYNQSPVSGVTDIWPV 445
QY 347 GVISYLSITCSPFAGSDRATLLNVLEGRVSWSSPMAHLSBDADKDF-IKATLQAPQA 405
Db 446 GVAFCLCTGISPPFVGENDRITLNMIRNVNVAPEETFTLSLSREARGFLIKVLQV--DRL 503
QY 406 RPSAAQCLSHFWFLKSPAEAEAFINTKQLKFLARSRWORSLSYK 452
Db 504 RPTABETLEHPWPKTOAKGAE---VSTDHLKFLSRRRWORSOISYK 547
RESULT 6
US-10-274-978-6
; Sequence 6, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00927-CIP-DIV
; CURRENT FILING DATE: 2002-10-22
; PRIOR FILING DATE: 2002-10-22
; PRIOR FILING DATE: 2001-05-17
; PRIOR FILING DATE: 09/711,134
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Human
US-10-274-978-6
Query Match 10.2%; Score 893; DB 4; Length 549;
Best Local Similarity 44.0%; Pred. No. 1.7e-45;
Matches 179; Conservative 79; Mismatches 135; Indels 14; Gaps 7;
QY 54 PSMQVTTIEDVQAQTGTAQFEAIIEDGDPQSPVTVYKDSYQVLVDSTRLSQQGGTYSVLV 113
Db 147 PRFSIMEDVEVGAGETARAVVVEGKPLDINWYKDEVLLETSSHVSVFVNECSLVV 206
QY 114 RHVASKDAGVYTCIAQNTGGQVLCABLLVLDGN---EPSEKQSHR-RKLHSPFYEVK 168
Db 207 LSTGAQGGVYCTAQNLAGVSCAKELAVHSAQTAMEVEGVGEDHRRGLSDFYDIH 266
QY 169 BEIGRGVFGVKRVQHKGNKILCAKFIPLRSRTRACAVRERDILALSHPLVTGLDQF 228
Db 267 QEIGRGAFSYLRIVERSSGLEFAKFIPLSQAKPKASAREALLARLQHDVCVLYFHEAF 326
QY 229 ETRKTLILILELCSBELLDRLYKGVVTEAEVKVYIQQLVEGLYHSHGVHLHDIKPS 288
Db 327 ERRGLVITVELC-TEELLERIAKPTVCESEIRAYMRQVLEGIHYHSHVHLHDVKPE 385
QY 289 NILMVHPA--REDIKICDFGAQNTPAELQFSGYSGPSPFVSPETIIQQNPVSEASDIWAM 346
Db 386 NLLVWDGAGQVQVRIQDFGNAQELTGEPOYCYGTPTPEFAVEIYNQSPVSGVTDIWPV 445
QY 347 GVISYLSITCSPFAGSDRATLLNVLEGRVSWSSPMAHLSBDADKDF-IKATLQAPQA 405
Db 446 GVAFCLCTGISPPFVGENDRITLNMIRNVNVAPEETFTLSLSREARGFLIKVLQV--DRL 503
QY 406 RPSAAQCLSHFWFLKSPAEAEAFINTKQLKFLARSRWORSLSYK 452
Db 504 RPTABETLEHPWPKTOAKGAE---VSTDHLKFLSRRRWORSOISYK 547

Db 446 GVAFCLCTGISPPFVGENDRITLNMIRNVNVAPEETFTLSLSREARGFLIKVLQV--DRL 503
QY 406 RPSAAQCLSHFWFLKSPAEAEAFINTKQLKFLARSRWORSLSYK 452
Db 504 RPTABETLEHPWPKTOAKGAE---VSTDHLKFLSRRRWORSOISYK 547
RESULT 7
US-09-858-664A-13
; Sequence 13, Application US/09858664A
; Patent No. 6482624
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00927-CIP
; CURRENT FILING DATE: 2001-05-17
; PRIOR FILING DATE: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-13
Query Match 6.8%; Score 592.5; DB 4; Length 414;
Best Local Similarity 34.5%; Pred. No. 1e-27;
Matches 145; Conservative 69; Mismatches 191; Indels 15; Gaps 6;
QY 53 PSMQVTTIEDVQAQTGTAQFEAIIEDGDPQSPVTVYKDSYQVLVDSTRLSQQGGT 107
Db 1 PPEFVPLSEVTCETGETVVLRCVCRGPKASITWKGPHEHTLNNDGHYSISYSDLGAT 60
QY 108 TYSVLVHVASDAGVYTCIAQNTGGQVLCABLLVLDGNPDSEKSHRRKLSHYEV 167
Db 61 ---LKVGVTTEDDGIYTCIAVNDMGSSASSASLVLPGE--MDGIMYTKDNFDSFVSE 115
QY 168 KEBIGRGVFGVKRVQHKGNKILCAKFIPLRSRTRACAVRERDILALSHPLVTGLDQ 227
Db 116 VAEIAGRGVFWKCKDQKGTKEAVATKFNKXLMKRDQVTHLGLIQLSHPLVGLD 175
QY 228 PETRKTLLILELCSSEELLDRYKGVVTEAEVKVYIQQLVEGLYHSHGVHLHDIKP 287
Db 176 FEPTSYILLVEMADQGRLLDCVWRWGLTEGKIRAHLEVLAVRYLHNCRIHLDPK 235
QY 288 SNILMVHP-AREDIKICDFGAQNTPAELQFSGYSGPSPFVSPETIIQQNPVSEASDIWAM 346
Db 236 ENILVDESIAKPTIKLADFGDAVQNTTVYIHOGLNFEFAAPEIILGNPVSLTSDTWSV 295
QY 347 GVISYLSITCSPFAGSDRATLLNVLEGRVSWSSPMAHLSBDADKDFIKATLQAPQA 406
Db 296 GVITYLLSGVGFDDSDVEETCLNICRLDFFDPDYFKGVSKAKFVCFLLQSDPAK 355
QY 407 PPSAAQCLSHFWFLKSPAEAEAFINTKQLKFLARSRWQ---RSLMSYKSLVWMSIPEL 463
Db 356 PSAAALAQEQW-LQAGNRSTGVLDTSRLTSFIERRKHQNDVPRISIKNLFQSLPRV 414
RESULT 8
US-10-274-978-14
; Sequence 14, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978

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; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Human
US-10-274-978-14

Query Match      6.8%; Score 592.5; DB 4; Length 414;
Best Local Similarity 34.5%; Pred. No. 1e-27;
Matches 145; Conservative 69; Mismatches 191; Indels 15; Gaps 6;

QY 53 PPSQVTTEDVQAGTGTGTAQFEALIEGDPQPSVWYKDSVQLVD-----STRLSQQQEGT 107
DB 1 PPFVIPLESEVTCETGETVILRCVCGRPKASITWKGPHEHTLNNDGHYSISYDLGEAT 60
QY 108 TYSVLRLHVASKDAGVYVTCIAQNTGGVLCVCAEALLVGLGDNEDPSEKSHRRKHLHSFYEV 167
DB 61 ---LKIVGVTTEDDGIYTCIAVNDMGSSASSASLRLVPG--MDGIMVTWKDNFDSFYSE 115
QY 168 KEIIGRGVGFVKVQVHKGKILCAAKFTPLSRTRACAYRERDTLAALSHPLVLTGLDQ 227
DB 116 VAEIIGRGVSVKCKDQKTKAVATKFNKLMKRDQVTHELGILQSLQHPILVGLDIT 175
QY 228 FETKTLILILELCSSEELDLRYKGVVTEAEVKYIQQLVEGLHYLHSHGVHLHDIKP 287
DB 176 FETPTSYILVLEMDQGRLLDCVVRWGSITGKIRAHLGVELEAVRYLHNCRIAHLDLKP 235
QY 288 SNILMHP-AREDIKICDFGFAQNTITPAELQFSQVSPFVSPEIIOQNPVSEASDIWAM 346
DB 236 ENILVDESIAKPTIKLADFGDAVOLNTYYIHQLGNPEFAPEIILGNPVSITSDTWSV 295
QY 347 GVYSYLSLTCSSPAGESDRATILNLVLEGRVSWSSPMAHLSEDAKDFIKATLQAPQAR 406
DB 296 GVITYVLLSGVSPFLDSDVEETCLNICRLDFFSPDDYFKGVSKAKFVCFLLQEDPAKR 355
QY 407 PSAAQCLSHPWFLKMPAEAEHFNKQLKFLARSWQ---RSLMSYKSLVWRSIP 463
DB 356 PSALALQEQW-LOANGRSTGVLDTSRLTSFIERRKHQNDVRPIRSIKNFLQSLRLPV 414

RESULT 9
US-08-826-267-2
; Sequence 2, Application US/08826267
; Patent No. 5994070
; GENERAL INFORMATION:
; APPLICANT: Streuli, Michel
; TITLE OF INVENTION: No. 5994070el TRIC Molecules and Uses Related Thereto
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,267
; FILING DATE: 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,214
; FILING DATE: 27 MARCH (1996)

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; ATTORNEY/AGENT INFORMATION:
; NAME: Amy B. Mandragoras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2860 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-826-267-2

Query Match      6.8%; Score 591.5; DB 2; Length 2860;
Best Local Similarity 34.7%; Pred. No. 1.4e-26;
Matches 145; Conservative 68; Mismatches 190; Indels 15; Gaps 6;

QY 53 PPSQVTTEDVQAGTGTGTAQFEALIEGDPQPSVWYKDSVQLVD-----STRLSQQQEGT 107
DB 2448 PPFVIPLESEVTCETGETVILRCVCGRPKASITWKGPHEHTLNNDGHYSISYDLGEAT 2507
QY 108 TYSVLRLHVASKDAGVYVTCIAQNTGGVLCVCAEALLVGLGDNEDPSEKSHRRKHLHSFYEV 167
DB 2508 ---LKIVGVTTEDDGIYTCIAVNDMGSSASSASLRLVPG--MDGIMVTWKDNFDSFYSE 2562
QY 168 KEIIGRGVGFVKVQVHKGKILCAAKFTPLSRTRACAYRERDTLAALSHPLVLTGLDQ 227
DB 2563 VAEIIGRGVSVKCKDQKTKAVATKFNKLMKRDQVTHELGILQSLQHPILVGLDIT 2622
QY 228 FETKTLILILELCSSEELDLRYKGVVTEAEVKYIQQLVEGLHYLHSHGVHLHDIKP 287
DB 2623 FETPTSYILVLEMDQGRLLDCVVRWGSITGKIRAHLGVELEAVRYLHNCRIAHLDLKP 2682
QY 288 SNILMHP-AREDIKICDFGFAQNTITPAELQFSQVSPFVSPEIIOQNPVSEASDIWAM 346
DB 2683 ENILVDESIAKPTIKLADFGDAVOLNTYYIHQLGNPEFAPEIILGNPVSITSDTWSV 2742
QY 347 GVYSYLSLTCSSPAGESDRATILNLVLEGRVSWSSPMAHLSEDAKDFIKATLQAPQAR 406
DB 2743 GVITYVLLSGVSPFLDSDVEETCLNICRLDFFSPDDYFKGVSKAKFVCFLLQEDPAKR 2802
QY 407 PSAAQCLSHPWFLKMPAEAEHFNKQLKFLARSWQ---RSLMSYKSLVWRSIP 461
DB 2803 PSALALQEQW-LOANGRSTGVLDTSRLTSFIERRKHQNDVRPIRSIKNFLQSLRLPV 2859

RESULT 10
US-09-858-664A-4
; Sequence 4, Application US/09858664A
; Patent No. 6482624
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL000927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-4

Query Match      6.1%; Score 531; DB 4; Length 279;
Best Local Similarity 39.5%; Pred. No. 2.8e-24;
Matches 111; Conservative 45; Mismatches 123; Indels 2; Gaps 1;

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QY 159 RKLHSFYEVKEIGRGVGFVGRVCHQKNGKILCAAKFIPILRSRTRAQAYR-ERDILAALS 217
Db 1 QKVSDFDIERLQSGFGQVFRLEKTRKRWAGFFKAYSACEKENIRQEISIMNCLH 60
QY 218 HPLVTGLDOPETRTKILILILELCSSEBLLDRLYRKG-VTEAEVKVYIQQLVEGLHYLH 276
Db 61 HPKLVQCVDAFEERANVMVLEISVSGGELFERIIDEFELTERECIKYMRQISEGVEYIH 120
QY 277 SHGVHLHDIKPSNLMVHPAREDIKICDFGAQNIITPAELQFSQYSGSPFVSPEIQQNP 336
Db 121 KQGVHLDLKPENIMCNKGTGRIKLDGLARLENAGSLKVLFGTPEFVAPEVINYEP 180
QY 337 VSEASDIWAGVISYLSLTCSPPAGESDRATLNLVLEGRVSWSSPMAHLSSEDAKDFIK 396
Db 181 ISVATDMWSIGVICYILVSGLSPPMGDNDNETLANVTSATWDFDDEAFDSDAKDFIS 240
QY 397 ATLQAPQARSACQILSHPWFLKMPAEBAHFINTKQLKFLARLSWQSLMSYKSI 454
Db 241 NLLKDKMKNRLDCTCQLQHPWLMKDTKQWAEAKLSKDKRMKKYKRWKQKTGNVRAI 298
RESULT 14
US-09-858-664A-18
; Sequence 18, Application US/09858664A
; Patent No. 6482424
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00927-CIP
; CURRENT APPLICATION NUMBER: US/09/858.664A
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-18
Query Match 5.8%; Score 509.5; DB 4; Length 508;
Best Local Similarity 25.5%; Pred. No. 1.2e-22;
Matches 125; Conservative 75; Mismatches 173; Indels 117; Gaps 5;
QY 48 PALGPPSNQVITIEDVQAQTGTGAQFEALIEGDPQSPVTVYKDSVOLVDSTRLSQQEGT 107
Db 18 PRAAMPQIIOPPEDQKVRAGESVELFGKVTGTQPTICTTMMKFRKQIQDSEHIKVENSEN 77
QY 108 TVSLVLRHVASKDAGVYICLAQNTGGVLCRAELVLG----- 145
Db 78 GSKLTILAAQEHCGCYTLLENKLGSRQAQVNLTVVDKPPAGTPCASIIRSSSLTSL 137
QY 146 -----G 146
Db 138 WYSSYDGGSAVQSYISIEIWDANKTKELATCRSTSFNVQDLLPDHEYKFRVRAINVG 197
QY 147 DNEP-----DSEKQ-----SHRRKLHSFYEVKEIG 172
Db 198 TSEPSQSESLTTVGEKPEPKMKWCQTDDEKEPEVDYRTVTINTEQKVSDFYDIERLG 257
QY 173 RGVFGFVKRVQKNGKILCAAKFIPILRSRTRAQAYR-ERDILAALSHPLVTGLDQFETR 231
Db 258 SGKFGQVFLVEKTRKRWAGFFKAYSACEKENIRQEISIMNCLHHPKLVQCVDAFEK 317
QY 232 KTLILILELCSSEBLLDRLYRKG-VTEAEVKVYIQQLVEGLHYLHSHGVHLHDIKPSNI 290
Db 318 ANIMVLEISVSGGELFERIIDEFELTERECIKYMRQISEGVEYIHKQIVHLDLKPENI 377
QY 291 LMVHPAREDIKICDFGAQNIITPAELQFSQYSGSPFVSPEIQQNPVSEASDIWAGVIS 350
Db 318 ANIMVLEISVSGGELFERIIDEFELTERECIKYMRQISEGVEYIHKQIVHLDLKPENI 377
QY 291 LMVHPAREDIKICDFGAQNIITPAELQFSQYSGSPFVSPEIQQNPVSEASDIWAGVIS 350

Db 378 MCVNKTGTRIKLDGLARLENAGSLKVLFGTPEFVAPEVINYEPISYATDMWSIGVIC 437
QY 351 YLSLTCSPPAGESDRATLNLVLEGRVSWSSPMAHLSSEDAKDFIKATLQAPQARPSAA 410
Db 438 YILVSGLSPPMGDNDNETLANVTSATWDFDDEAFDSDAKDFISNLLKKDKMKNRLDCT 497
QY 411 QCLSHPWFLK 420
Db 498 QCLQHPWLMK 507
RESULT 15
US-10-274-978-19
; Sequence 19, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Human
US-10-274-978-19
Query Match 5.8%; Score 509.5; DB 4; Length 508;
Best Local Similarity 25.5%; Pred. No. 1.2e-22;
Matches 125; Conservative 75; Mismatches 173; Indels 117; Gaps 5;
QY 48 PALGPPSNQVITIEDVQAQTGTGAQFEALIEGDPQSPVTVYKDSVOLVDSTRLSQQEGT 107
Db 18 PRAAMPQIIOPPEDQKVRAGESVELFGKVTGTQPTICTTMMKFRKQIQDSEHIKVENSEN 77
QY 108 TVSLVLRHVASKDAGVYICLAQNTGGVLCRAELVLG----- 145
Db 78 GSKLTILAAQEHCGCYTLLENKLGSRQAQVNLTVVDKPPAGTPCASIIRSSSLTSL 137
QY 146 -----G 146
Db 138 WYSSYDGGSAVQSYISIEIWDANKTKELATCRSTSFNVQDLLPDHEYKFRVRAINVG 197
QY 147 DNEP-----DSEKQ-----SHRRKLHSFYEVKEIG 172
Db 198 TSEPSQSESLTTVGEKPEPKMKWCQTDDEKEPEVDYRTVTINTEQKVSDFYDIERLG 257
QY 173 RGVFGFVKRVQKNGKILCAAKFIPILRSRTRAQAYR-ERDILAALSHPLVTGLDQFETR 231
Db 258 SGKFGQVFLVEKTRKRWAGFFKAYSACEKENIRQEISIMNCLHHPKLVQCVDAFEK 317
QY 232 KTLILILELCSSEBLLDRLYRKG-VTEAEVKVYIQQLVEGLHYLHSHGVHLHDIKPSNI 290
Db 318 ANIMVLEISVSGGELFERIIDEFELTERECIKYMRQISEGVEYIHKQIVHLDLKPENI 377
QY 291 LMVHPAREDIKICDFGAQNIITPAELQFSQYSGSPFVSPEIQQNPVSEASDIWAGVIS 350
Db 378 MCVNKTGTRIKLDGLARLENAGSLKVLFGTPEFVAPEVINYEPISYATDMWSIGVIC 437
QY 351 YLSLTCSPPAGESDRATLNLVLEGRVSWSSPMAHLSSEDAKDFIKATLQAPQARPSAA 410
Db 438 YILVSGLSPPMGDNDNETLANVTSATWDFDDEAFDSDAKDFISNLLKKDKMKNRLDCT 497
QY 411 QCLSHPWFLK 420

Wed Apr 28 15:17:53 2004

Db 498 QCLQHPWLMK 507

Search completed: April 23, 2004, 15:12:06
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:11:23 ; Search time 59 Seconds
(without alignments)
7802.224 Million cell updates/sec

Title: US-10-697-263-2

Perfect score: 8740

Sequence: 1 MGCCRLGCGCSVAHSVSG.....RNREKRALLYKRNHLAQVR 1665

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	8740	100.0	1665	12	US-10-697-263-2
3	8727	99.9	1665	12	US-10-415-011-22
4	8423	96.4	2630	13	US-10-077-130-2
5	8423	96.4	7968	13	US-10-077-130-5
6	8417	96.3	2596	14	US-10-307-019-6
7	8403	96.1	1618	12	US-10-182-243-46
8	8399	96.1	1610	14	US-10-307-019-4
9	7069	80.9	1351	14	US-10-307-019-1
10	4533	51.9	871	16	US-10-311-034-20
11	4529	51.8	871	14	US-10-307-019-7
12	2447.5	28.0	548	14	US-10-307-019-8
13	2415.5	27.6	548	14	US-10-307-019-9
14	2045	23.4	390	12	US-10-425-114-37530
15	1973	22.6	2380	12	US-10-333-314-18

ALIGNMENTS

RESULT 1

US-09-858-664A-2
; Sequence 2, Application US/09858664A
; Patent No. US20020072491A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-2

Query Match 100.0%; Score 8740; DB 9; Length 1665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGCCRLGCGCSVAHSVSGGLTNHPSVCGWHPCGLCGWGGGLHSSLPALPQPPSMQVTI 60
Db 1 MGCCRLGCGCSVAHSVSGGLTNHPSVCGWHPCGLCGWGGGLHSSLPALPQPPSMQVTI 60
Qy 61 EDVQAQTGTAQFEAIIIEGDPQPSVTWYKDSVQLVDSVTRLSQQQEGTTSYLVLRHASKD 120
Db 61 EDVQAQTGTAQFEAIIIEGDPQPSVTWYKDSVQLVDSVTRLSQQQEGTTSYLVLRHASKD 120
Qy 121 AGVYTCLAQNTGGQVLCRAELLVLGDDNEPDKSEKSHRKLHSFYEVKEETGRGVFGVK 180
Db 121 AGVYTCLAQNTGGQVLCRAELLVLGDDNEPDKSEKSHRKLHSFYEVKEETGRGVFGVK 180

16 1973 22.6 3208 15 US-10-210-130-38 Sequence 38, Appl
17 1967.5 22.5 3268 15 US-10-379-381-2 Sequence 2, Appl
18 1931 22.1 3252 15 US-10-210-130-36 Sequence 36, Appl
19 1913 21.9 2231 15 US-10-379-381-5 Sequence 5, Appl
20 1864 21.3 3262 15 US-10-379-381-4 Sequence 4, Appl
21 1746.5 20.0 3186 15 US-10-210-130-34 Sequence 34, Appl
22 1173 13.4 846 9 US-09-858-664A-3 Sequence 3, Appl
23 1173 13.4 846 12 US-10-697-263-4 Sequence 4, Appl
24 893 10.2 549 9 US-09-858-664A-5 Sequence 5, Appl
25 893 10.2 549 12 US-10-697-263-6 Sequence 6, Appl
26 702.5 8.0 1398 15 US-10-369-493-5014 Sequence 5014, Ap
27 632.5 7.2 282 11 US-10-210-130-40 Sequence 40, Appl
28 607 6.9 127 11 US-09-864-408A-8948 Sequence 8948, Ap
29 592.5 6.8 414 9 US-09-858-664A-13 Sequence 13, Appl
30 592.5 6.8 414 12 US-10-697-263-14 Sequence 14, Appl
31 592.5 6.8 2861 12 US-10-182-936A-108 Sequence 108, App
32 592.5 6.8 2861 15 US-10-374-979-108 Sequence 108, App
33 592.5 6.8 2861 15 US-10-331-496A-89 Sequence 89, Appl
34 592.5 6.8 3038 10 US-09-863-776-62 Sequence 62, Appl
35 561.5 6.4 416 9 US-09-925-299-887 Sequence 887, App
36 561.5 6.4 416 10 US-09-925-299-887 Sequence 887, App
37 551 6.3 520 12 US-10-425-114-54134 Sequence 54134, A
38 531 6.1 279 9 US-09-858-664A-4 Sequence 4, Appl
39 531 6.1 279 12 US-10-697-263-5 Sequence 5, Appl
40 526 6.0 468 12 US-10-425-114-54120 Sequence 54120, A
41 523.5 6.0 2783 15 US-10-369-493-6344 Sequence 6344, Ap
42 521 6.0 298 9 US-09-858-664A-17 Sequence 17, Appl
43 521 6.0 298 12 US-10-697-263-18 Sequence 18, Appl
44 509.5 5.8 508 9 US-09-858-664A-18 Sequence 18, Appl
45 509.5 5.8 508 12 US-10-697-263-19 Sequence 19, Appl

QY 181 RVQKGNKILCAAKFIPLRSTRQAAYRERDILAAALSHPLVTGLLDQFETKTLILLEL 240
DB 181 RVQKGNKILCAAKFIPLRSTRQAAYRERDILAAALSHPLVTGLLDQFETKTLILLEL 240
QY 241 CSSELDRLRYKGVVTEAVKVIYIQLVEGLHYLHSHGVHLHDIKPSNIMLWHPAREDI 300
DB 241 CSSELDRLRYKGVVTEAVKVIYIQLVEGLHYLHSHGVHLHDIKPSNIMLWHPAREDI 300
QY 301 KICDFGAQNTTFAELQFQYGSPEFVSPPIIQONFVSEASDIWANGVISYLSLTCSSPF 360
DB 301 KICDFGAQNTTFAELQFQYGSPEFVSPPIIQONFVSEASDIWANGVISYLSLTCSSPF 360
QY 361 AGESDRATLNLVLEGRVSWSPYAAHLSEDAKDFIKATLQRAQAPPSAAQCSLHPWELK 420
DB 361 AGESDRATLNLVLEGRVSWSPYAAHLSEDAKDFIKATLQRAQAPPSAAQCSLHPWELK 420
QY 421 SMPAEBAHFINTKOLKELLARSWORSLMSYKILVMRSIPPELLRGPDSPSLGVARHLK 480
DB 421 SMPAEBAHFINTKOLKELLARSWORSLMSYKILVMRSIPPELLRGPDSPSLGVARHLK 480
QY 481 RDTGSSSSSSSSDNLAPARAKSLPPSPVTHSPHLLHPRGFTLRPSASLPEAEASERST 540
DB 481 RDTGSSSSSSSSDNLAPARAKSLPPSPVTHSPHLLHPRGFTLRPSASLPEAEASERST 540
QY 541 EAPAPPASPGAGPAAQGCVPKHSVIRSLFYHQAGESPEHGALAPGRRRHPARRHLK 600
DB 541 EAPAPPASPGAGPAAQGCVPKHSVIRSLFYHQAGESPEHGALAPGRRRHPARRHLK 600
QY 601 GGYIAGALPGLRBLPMLHRVLEBAAREEOATLLAKAPSFETALRILPASGTHLAPGSHS 660
DB 601 GGYIAGALPGLRBLPMLHRVLEBAAREEOATLLAKAPSFETALRILPASGTHLAPGSHS 660
QY 661 LEHDSPTTPRPSSEACGEAQLRPSAPGGAPTRDMGHQPGSKQLPSTGHPGTAQPERPS 720
DB 661 LEHDSPTTPRPSSEACGEAQLRPSAPGGAPTRDMGHQPGSKQLPSTGHPGTAQPERPS 720
QY 721 PDSFWGQPAFCFHPKQSAQECSPHPAVAPCPGSPFPFGCKEAPLVPSSPFLGQQA 780
DB 721 PDSFWGQPAFCFHPKQSAQECSPHPAVAPCPGSPFPFGCKEAPLVPSSPFLGQQA 780
QY 781 PPAPAKASPLDSKMGDGLSLGRPKPGPCSPGASQASSQVSSLRVSSQVGTPEP 840
DB 781 PPAPAKASPLDSKMGDGLSLGRPKPGPCSPGASQASSQVSSLRVSSQVGTPEP 840
QY 841 PSIDAEGWTCBAEDLSDSTPLRPOBOVTMRKFSLGGGGYAGVAGTGFAGGDAGGM 900
DB 841 PSIDAEGWTCBAEDLSDSTPLRPOBOVTMRKFSLGGGGYAGVAGTGFAGGDAGGM 900
QY 901 LGQGFMMARIAMVSSQEEBEEAEASQSEBQAEARAEPLQVARSAPPEVGRAPTR 960
DB 901 LGQGFMMARIAMVSSQEEBEEAEASQSEBQAEARAEPLQVARSAPPEVGRAPTR 960
QY 961 SSPEPTWEDIGQVSLVQIRDLSDGDAEADTISLDISEVDPAVNLSDLYDKYLPPEFM 1020
DB 961 SSPEPTWEDIGQVSLVQIRDLSDGDAEADTISLDISEVDPAVNLSDLYDKYLPPEFM 1020
QY 1021 IFRKVPKSAQPEPPSPNAEBELAEFPPTWMPGELGPHAGLEITEESDVEDALLAEAAV 1080
DB 1021 IFRKVPKSAQPEPPSPNAEBELAEFPPTWMPGELGPHAGLEITEESDVEDALLAEAAV 1080
QY 1081 GRKXKMSPPSRSLFHPGRHLPLDEPAELGLRERVKASVEHLSRILKGRPEGEKEGPPR 1140
DB 1081 GRKXKMSPPSRSLFHPGRHLPLDEPAELGLRERVKASVEHLSRILKGRPEGEKEGPPR 1140
QY 1141 KPGLASFRSLGKSWDRAPTFIRELSDETIVVGGSVTLACQVSAQPAQATWSKOGAPL 1200
DB 1141 KPGLASFRSLGKSWDRAPTFIRELSDETIVVGGSVTLACQVSAQPAQATWSKOGAPL 1200
QY 1201 ESSSRVLISATLKNFOLLITLVVAEDDLGVYTCVSNALGTVTVTGVLKKAERSSSPCP 1260
DB 1201 ESSSRVLISATLKNFOLLITLVVAEDDLGVYTCVSNALGTVTVTGVLKKAERSSSPCP 1260
QY 1261 DIGEVADGVLLVWKPVESYGPVTYIVQCSLEGGSWTTLASDIPDCCVLTSLKSRGGTYT 1320

DB 1261 DIGEVADGVLLVWKPVESYGPVTYIVQCSLEGGSWTTLASDIPDCCVLTSLKSRGGTYT 1320
QY 1321 FRTACVSKAGMCPYSPSPQVLLGSPSHLASEEESQBSAQPLPSTKTFAQTQIORGRF 1380
DB 1321 FRTACVSKAGMCPYSPSPQVLLGSPSHLASEEESQBSAQPLPSTKTFAQTQIORGRF 1380
QY 1381 SVVRQWEKASGRALAAKIIIPYHPKDKTAVLRVEYALKGLRHPHLAQHAAAYLSPRHLVL 1440
DB 1381 SVVRQWEKASGRALAAKIIIPYHPKDKTAVLRVEYALKGLRHPHLAQHAAAYLSPRHLVL 1440
QY 1441 ILELCGPELLPCLAEARASYSESEVKYLMOWLSATQVLRNQHILHDLRSENMIITEYN 1500
DB 1441 ILELCGPELLPCLAEARASYSESEVKYLMOWLSATQVLRNQHILHDLRSENMIITEYN 1500
QY 1501 LKWDVLDGNAQSLQSKVLPDSKFKDYLETMAPELLEGQGAVPQTDIWAIGVTAFIMLSA 1560
DB 1501 LKWDVLDGNAQSLQSKVLPDSKFKDYLETMAPELLEGQGAVPQTDIWAIGVTAFIMLSA 1560
QY 1561 EYVPSSEGARDLQRLKGLVRLSCYAGLSGGAFAFLRSTLCAQPKGRPCASSCLOC PW 1620
DB 1561 EYVPSSEGARDLQRLKGLVRLSCYAGLSGGAFAFLRSTLCAQPKGRPCASSCLOC PW 1620
QY 1621 LTEEGPACSRPAPVTFPTARLRVFNVRNREKRALLYKRNHIAQVR 1665
DB 1621 LTEEGPACSRPAPVTFPTARLRVFNVRNREKRALLYKRNHIAQVR 1665

RESULT 2

US-10-697-263-2
; Sequence 2, Application US/10697263
; Publication No. US20040063142A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000927-CIP-DIV2
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 10/274,978
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-697-263-2

Query Match 100.0%; Score 8740; DB 12; Length 1665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCCRLGCGGCSVAHSVSGGLTNHPSPVCGWHPGLCGWGGGLHSSLPALPGPPSMQVTI 60
DB 1 MCCRLGCGGCSVAHSVSGGLTNHPSPVCGWHPGLCGWGGGLHSSLPALPGPPSMQVTI 60
QY 61 EDVQAQTGTAQFAEALIEGDQPSPVTVTKOSVQLVDSTRLSQQQEGTYSVLVHVASKD 120
DB 61 EDVQAQTGTAQFAEALIEGDQPSPVTVTKOSVQLVDSTRLSQQQEGTYSVLVHVASKD 120
QY 121 AGVYTCLAQNTGGQVLCXAEILLVITGGNENPDEKSHRRKLHSPYEVKEBIGRVGFVK 180
DB 121 AGVYTCLAQNTGGQVLCXAEILLVITGGNENPDEKSHRRKLHSPYEVKEBIGRVGFVK 180
QY 181 RVQKGNKILCAAKFIPLRSTRQAAYRERDILAAALSHPLVTGLLDQFETKTLILLEL 240
DB 181 RVQKGNKILCAAKFIPLRSTRQAAYRERDILAAALSHPLVTGLLDQFETKTLILLEL 240

QY 241 CSSELDRLVRKGVVTEAEVKVYIQOLVEGLHYLHSHGVHLHLDIKPSNLMVHPAREDI 300
DB 241 CSSELDRLVRKGVVTEAEVKVYIQOLVEGLHYLHSHGVHLHLDIKPSNLMVHPAREDI 300
QY 301 KICDFGFAQNTITPAELOFSQYSGSEFVSPETIQONPVSEASDIWAMGVISYLSLTCSPP 360
DB 301 KICDFGFAQNTITPAELOFSQYSGSEFVSPETIQONPVSEASDIWAMGVISYLSLTCSPP 360
QY 361 AGESDRATLLNVLEGRVSWSPMAHLSEDAKOFIKATLORAPQAPSPAAQCLSHFWFLK 420
DB 361 AGESDRATLLNVLEGRVSWSPMAHLSEDAKOFIKATLORAPQAPSPAAQCLSHFWFLK 420
QY 421 SMPAEAAHFINTKOLKFLAASRWORSIMSYKSTILVWRSIPELLRGPDPSPSIVARHLK 480
DB 421 SMPAEAAHFINTKOLKFLAASRWORSIMSYKSTILVWRSIPELLRGPDPSPSIVARHLK 480
QY 481 RDTGSSSSSSSSSNEELAPARAKSLPPSPVTHSPLLHPRGFTURPSASIPPEBAEASERT 540
DB 481 RDTGSSSSSSSSSNEELAPARAKSLPPSPVTHSPLLHPRGFTURPSASIPPEBAEASERT 540
QY 541 EAPAPPASPEGAGPPAAGCQVPRHSVIRSLFYHQGESPEHGALAPGSRHHPARRRHLLK 600
DB 541 EAPAPPASPEGAGPPAAGCQVPRHSVIRSLFYHQGESPEHGALAPGSRHHPARRRHLLK 600
QY 601 GGYTAGALPGLURBIMEHRVLEBAABEQATLLAKAPSPETALRPLASGTHLAPGHSHS 660
DB 601 GGYTAGALPGLURBIMEHRVLEBAABEQATLLAKAPSPETALRPLASGTHLAPGHSHS 660
QY 661 LEHDSPTSPRPSSEACGEAORLPAPSGGAPIRDMGHPQSGKOLPSTGGHPGTAQPERPS 720
DB 661 LEHDSPTSPRPSSEACGEAORLPAPSGGAPIRDMGHPQSGKOLPSTGGHPGTAQPERPS 720
QY 721 PDSWQGPAPCHPKQGSAPQEGGSPHAPVAPCPGSPFPFGSCKEAPLVPSPFFLGQPOA 780
DB 721 PDSWQGPAPCHPKQGSAPQEGGSPHAPVAPCPGSPFPFGSCKEAPLVPSPFFLGQPOA 780
QY 781 PPAKASAPPLDSDXMGPGDLSLGRPKPGPCSPGSGASQSSQVSSSLRVGSSOVGTGEG 840
DB 781 PPAKASAPPLDSDXMGPGDLSLGRPKPGPCSPGSGASQSSQVSSSLRVGSSOVGTGEG 840
QY 841 PSLDAEGWTOABDLSDSTPTLQRPQOVNTRKPSLGGRCGYAGVAGYGTTFAGGDAGM 900
DB 841 PSLDAEGWTOABDLSDSTPTLQRPQOVNTRKPSLGGRCGYAGVAGYGTTFAGGDAGM 900
QY 901 LGQPMWARIWAYSQGESEEBEQEAREASQSEBQEQARABSPLOVARSAPVPEVGRAPTR 960
DB 901 LGQPMWARIWAYSQGESEEBEQEAREASQSEBQEQARABSPLOVARSAPVPEVGRAPTR 960
QY 961 SSPPTPWEDIGQVSLVQIRDLSDGAEADTISLDSIVDPAYLNSLDYDIKYLFFPEPM 1020
DB 961 SSPPTPWEDIGQVSLVQIRDLSDGAEADTISLDSIVDPAYLNSLDYDIKYLFFPEPM 1020
QY 1021 IFRKVPKSAQEPSPMAEELAEFPPTWPMGELPHAGLEITRESEDDVALLAEAAV 1080
DB 1021 IFRKVPKSAQEPSPMAEELAEFPPTWPMGELPHAGLEITRESEDDVALLAEAAV 1080
QY 1081 GRKRWSSPSLSLFFHFGRLPLDEPAELGLRERVKASVEHISRIILKGRPEGLEKEGPPR 1140
DB 1081 GRKRWSSPSLSLFFHFGRLPLDEPAELGLRERVKASVEHISRIILKGRPEGLEKEGPPR 1140
QY 1141 KKPGLASFLSLGSKSWDRAPTFLELSDETIVVIGQSVTLACQVSAQPAQATWSKDGAPL 1200
DB 1141 KKPGLASFLSLGSKSWDRAPTFLELSDETIVVIGQSVTLACQVSAQPAQATWSKDGAPL 1200
QY 1201 ESSSRVLISATLKNFOLLITLIVVAEDLGVYTCVSNALGTVTITGLVKAERPPSSPCP 1260
DB 1201 ESSSRVLISATLKNFOLLITLIVVAEDLGVYTCVSNALGTVTITGLVKAERPPSSPCP 1260
QY 1261 DIGEVYADGVLLVWKPVSQGVPTIYVQCSLEGGSWTTLASDIFDCCYLTSLKSRGTTT 1320
DB 1261 DIGEVYADGVLLVWKPVSQGVPTIYVQCSLEGGSWTTLASDIFDCCYLTSLKSRGTTT 1320

QY 1321 FRTACVSKAGMGYSPPSEBOVLLGGPSHLASEBESQGRSAQBLPSTTKTFAFOTQIORGRF 1380
DB 1321 FRTACVSKAGMGYSPPSEBOVLLGGPSHLASEBESQGRSAQBLPSTTKTFAFOTQIORGRF 1380
QY 1381 SVVROCKEASGALAAKIIPIYHPKDKTAVLREYEALKGLRHPHLAQLHAAYLSPRHLVL 1440
DB 1381 SVVROCKEASGALAAKIIPIYHPKDKTAVLREYEALKGLRHPHLAQLHAAYLSPRHLVL 1440
QY 1441 ILELCSGPPELLPCLABRASYSSEVKOYLWOMLSATQYILHNOHILHLDURSENMIITEYN 1500
DB 1441 ILELCSGPPELLPCLABRASYSSEVKOYLWOMLSATQYILHNOHILHLDURSENMIITEYN 1500
QY 1501 LLKVVLDLGNAAQSLSQEKVLPDSKFKDYLETMAPELLEGQGVQPTDIIWAIGVTAFTIMLSA 1560
DB 1501 LLKVVLDLGNAAQSLSQEKVLPDSKFKDYLETMAPELLEGQGVQPTDIIWAIGVTAFTIMLSA 1560
QY 1561 EYPVSSSGARDLQRLKGLVRLSRVAGLSGAVAFIRSTICAQWGRPCASSCLOCQW 1620
DB 1561 EYPVSSSGARDLQRLKGLVRLSRVAGLSGAVAFIRSTICAQWGRPCASSCLOCQW 1620
QY 1621 LITEGPACSPAPVPTPTARLRFVVRNREKRALLYKRNHLAQVR 1665
DB 1621 LITEGPACSPAPVPTPTARLRFVVRNREKRALLYKRNHLAQVR 1665

RESULT 3

US-10-415-011-22
; Sequence 22, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah K.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAPALIA, April J.A.
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: BOROMSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; PRIOR FILING DATE: 2003-04-18
; PRIOR FILING DATE: 2001-10-20
; PRIOR FILING DATE: 2001-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 2000-11-03
; PRIOR FILING DATE: 2000-11-09
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR APPLICATION NUMBER: US 60/249,565

; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-130-2

Query Match 96.4%; Score 8423; DB 13; Length 2630;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 53 PPSQVITIEDVQAGTGAQPEALIEGDPQSVTWYKDSVOLVDSITLSQQQEGTYSVLV 112
Db 1018 PPSQVITIEDVQAGTGAQPEALIEGDPQSVTWYKDSVOLVDSITLSQQQEGTYSVLV 1077
QY 113 LRHVASKDAGVYTCLAQNTGQVCKAEILLVLDGNEPDSEKSHRKLHSFVYKVEIG 172
Db 1078 LRHVASKDAGVYTCLAQNTGQVCKAEILLVLDGNEPDSEKSHRKLHSFVYKVEIG 1137
QY 173 RGVFGFVKRVQHKNGKILCAAKFIPLRSRTAQAYRERDILAAALSHPLVTGLLDQFETR 232
Db 1138 RGVFGFVKRVQHKNGKILCAAKFIPLRSRTAQAYRERDILAAALSHPLVTGLLDQFETR 1197
QY 233 TLIIILELCSSEELDLRYRGVVTAEARKYIIOQLVEGLHYLHSHGVHLHDIKPSNIM 292
Db 1198 TLIIILELCSSEELDLRYRGVVTAEARKYIIOQLVEGLHYLHSHGVHLHDIKPSNIM 1257
QY 293 VHPAREDIKICDFGFAQNTIPEALQFSGYSGPEFVSPPIIQONPVSEASDIWANGVISYL 352
Db 1258 VHPAREDIKICDFGFAQNTIPEALQFSGYSGPEFVSPPIIQONPVSEASDIWANGVISYL 1317
QY 353 SLTCSPPAGSDRATLNLVLEGRVSWSSPMAHLSEDAKFIKATLQAPQAPPSAAQC 412
Db 1318 SLTCSPPAGSDRATLNLVLEGRVSWSSPMAHLSEDAKFIKATLQAPQAPPSAAQC 1377
QY 413 LSHPFKLSMAEAEAHFNTKQLFLARSQWLSMSYKILVMSIPELLRPPDPS 472
Db 1378 LSHPFKLSMAEAEAHFNTKQLFLARSQWLSMSYKILVMSIPELLRPPDPS 1437
QY 473 LGVARHLCRDTGGSSSSSSSDNELAPPARAKSLPPSPVTHSLPHRPFGLRPSASLPEE 532
Db 1438 LGVARHLCRDTGGSSSSSSSDNELAPPARAKSLPPSPVTHSLPHRPFGLRPSASLPEE 1497
QY 533 AEASRSTAPAPASPGAGPPAAQGCVPKHSVIRSLFYHQAGSPHGHGALAPGSRHP 592
Db 1498 AEASRSTAPAPASPGAGPPAAQGCVPKHSVIRSLFYHQAGSPHGHGALAPGSRHP 1557
QY 593 ARRHLLKGGYIAGALPGLREPLMEHVRVLEBEAAREEQATLLAKAPSETALRLPASGTH 652
Db 1558 ARRHLLKGGYIAGALPGLREPLMEHVRVLEBEAAREEQATLLAKAPSETALRLPASGTH 1617
QY 653 LAPGSHLSLEHDSPTPRPSSEACGEAQLPSAPSGGAPIRDMGHPQSKQLPSTGGHPG 712
Db 1618 LAPGSHLSLEHDSPTPRPSSEACGEAQLPSAPSGGAPIRDMGHPQSKQLPSTGGHPG 1677
QY 713 TQAPERPDSPWGPAPFCHPKQGSAPQEGCSHPAVAPCPGSPFPGSCKEAPLPVPS 772
Db 1678 TQAPERPDSPWGPAPFCHPKQGSAPQEGCSHPAVAPCPGSPFPGSCKEAPLPVPS 1737
QY 773 PFLGQFAPPAPAKASPLDQXMGFDISLPGRPKPGPCSPFGSASQASSQVSLRVGS 832
Db 1738 PFLGQFAPPAPAKASPLDQXMGFDISLPGRPKPGPCSPFGSASQASSQVSLRVGS 1797
QY 833 SOVGTEPGSLDAEGWTEAEPLDSTPTLQRPQVQVTRKFSLGGRGYAGVAGYGTFA 892
Db 1798 SOVGTEPGSLDAEGWTEAEPLDSTPTLQRPQVQVTRKFSLGGRGYAGVAGYGTFA 1857
QY 893 FGGDAGGMLGQGMWARIWAYSQSEEEQAEARASQSEEQAEARASPLPQVSARVP 952
Db 1858 FGGDAGGMLGQGMWARIWAYSQSEEEQAEARASQSEEQAEARASPLPQVSARVP 1917

953 EVGRAPTRSSPEPTWEDIGQVSLVQIRDLSDGDAFAAATISLIDISEVDPAYNLSDLVDI 1012
1918 EVGRAPTRSSPEPTWEDIGQVSLVQIRDLSDGDAFAAATISLIDISEVDPAYNLSDLVDI 1977
QY 1013 KYLPEEFMIERKVPKSAQPEPPSMAEELAEFFPEPTWPMQELCPHAGLEITTESEVD 1072
1978 KYLPEEFMIERKVPKSAQPEPPSMAEELAEFFPEPTWPMQELCPHAGLEITTESEVD 2037
QY 1073 ALLAAAVGRKRWSSPSRSLFHPFGRHLPLDEPAELGLRERVKASVEHISRIILKGRPEG 1132
2038 ALLAAAVGRKRWSSPSRSLFHPFGRHLPLDEPAELGLRERVKASVEHISRIILKGRPEG 2097
QY 1133 LRKEGPPRKPCGLASFRSLGKSWDRAPTFELRELSDETIVLGQSVTLACQVSAQPAQAAT 1192
2098 LRKEGPPRKPCGLASFRSLGKSWDRAPTFELRELSDETIVLGQSVTLACQVSAQPAQAAT 2157
QY 1193 WSKDAPLESSSRVLISATLKNFQLLTILVVAEDLGYTCSVSNALGTVTGVLRAE 1252
2158 WSKDAPLESSSRVLISATLKNFQLLTILVVAEDLGYTCSVSNALGTVTGVLRAE 2217
QY 1253 RPSSSPCPDIGVYADGVLVWKPVESYCPVTYIQCSELEGGSWTTLASDIFDCCVLTSK 1312
2218 RPSSSPCPDIGVYADGVLVWKPVESYCPVTYIQCSELEGGSWTTLASDIFDCCVLTSK 2277
QY 1313 LSRGGTYTTFRTACVSKAGMPYSSPSEQVLLGPGSHLASEEESQGRSAQPLSTKTFAFQ 1372
2278 LSRGGTYTTFRTACVSKAGMPYSSPSEQVLLGPGSHLASEEESQGRSAQPLSTKTFAFQ 2337
QY 1373 TQIQGRFVSVQCKEKASGRALAAKIIPYHPKDKTAVLREYEAALKGLRPHLAQHAAY 1432
2338 TQIQGRFVSVQCKEKASGRALAAKIIPYHPKDKTAVLREYEAALKGLRPHLAQHAAY 2397
QY 1433 LSPRHVLVLELCSGPPELLPCLAEARASYSESEVKDYLMQMLSATQVYLNQHLHLDRSE 1492
2398 LSPRHVLVLELCSGPPELLPCLAEARASYSESEVKDYLMQMLSATQVYLNQHLHLDRSE 2457
QY 1493 NMIITEYNLLKVVLDGNAOSLSQEKVLPDSKFKDYLETWAPELLEGGQAVPQTDIWAIGV 1552
2458 NMIITEYNLLKVVLDGNAOSLSQEKVLPDSKFKDYLETWAPELLEGGQAVPQTDIWAIGV 2517
QY 1553 TAFIMLSAEVPSVSESGARDLQRLKGLVRLSRVAGLSGGAVAFURSTLCAQPWGRPCA 1612
2518 TAFIMLSAEVPSVSESGARDLQRLKGLVRLSRVAGLSGGAVAFURSTLCAQPWGRPCA 2577
QY 1613 SSCLOCPWLTEEGPACSRPAPVTFPTARLVFVRNREKRALLYKHNLAQVR 1665
2578 SSCLOCPWLTEEGPACSRPAPVTFPTARLVFVRNREKRALLYKHNLAQVR 2630

RESULT 5
US-10-077-130-5
; Sequence 5, Application US/10077130
; Publication No. US20020168742A1
; GENERAL INFORMATION:
; APPLICANT: Kapellier-Libermann, Rosana
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MEI2001-047P1RCPI(M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-130-5

Query Match 96.4%; Score 8423; DB 13; Length 7968;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	53	PPSMQVTIEDVQAQTGGTAQFAEIIIEGDPQFSYTWYKDSVQLVDSTRLSQQQEGTTSYSLV	112
Db	6356	PPSMQVTIEDVQAQTGGTAQFAEIIIEGDPQFSYTWYKDSVQLVDSTRLSQQQEGTTSYSLV	6415
QY	113	LHHVASKDAGVYTCIAQNTGGVLCRAELIIVTGGDNEPDSEKOSHRKHLHSFYEVKSEIG	172
Db	6416	LHHVASKDAGVYTCIAQNTGGVLCRAELIIVTGGDNEPDSEKOSHRKHLHSFYEVKSEIG	6475
QY	173	RGVFGFVKRVQHKGNKILCAAKTFLRSRTRAQYRERDILAAALSHPLVTGLLQDFETR	232
Db	6476	RGVFGFVKRVQHKGNKILCAAKTFLRSRTRAQYRERDILAAALSHPLVTGLLQDFETR	6535
QY	233	TLIILILECSSEELIDRLYKGVVTVAEVKKVILQQLVEGLHYLHSHGVHLHDIKPSNLM	292
Db	6536	TLIILILECSSEELIDRLYKGVVTVAEVKKVILQQLVEGLHYLHSHGVHLHDIKPSNLM	6595
QY	293	VHPAREDKICDGFQAQNIPTAELQPSQXGSPFVSPEIIQQNPVSEASDIWAMGVISYL	352
Db	6596	VHPAREDKICDGFQAQNIPTAELQPSQXGSPFVSPEIIQQNPVSEASDIWAMGVISYL	6655
QY	353	SLTCSPPAGESDRATILNVLEGRVSWSSPMAHLSEDAKDFIKATLQRAQAPRPSAAQC	412
Db	6656	SLTCSPPAGESDRATILNVLEGRVSWSSPMAHLSEDAKDFIKATLQRAQAPRPSAAQC	6715
QY	413	LSHPWFLKSMPEAEHAFINTKQLFLARSRWORSIMSYKSLVNRSPPELLRPPDPS	472
Db	6716	LSHPWFLKSMPEAEHAFINTKQLFLARSRWORSIMSYKSLVNRSPPELLRPPDPS	6775
QY	473	LOVAHRLCRDTGCGSSSSSSSSDDELAPPARAKSLPSPVTHSPHLLHPGFLRPSASLPEE	532
Db	6776	LOVAHRLCRDTGCGSSSSSSSSDDELAPPARAKSLPSPVTHSPHLLHPGFLRPSASLPEE	6835
QY	533	AEASRSTEARPAPASPEGAGPAAQGVPRHSVIRSLFYHOAGSPBHGALAPGSRHRP	592
Db	6836	AEASRSTEARPAPASPEGAGPAAQGVPRHSVIRSLFYHOAGSPBHGALAPGSRHRP	6895
QY	593	ARRHLKGGYIACALPGLREPMYHRVLEEEAAREQATLLAKAPSETALRPLASGTH	652
Db	6896	ARRHLKGGYIACALPGLREPMYHRVLEEEAAREQATLLAKAPSETALRPLASGTH	6955
QY	653	LAPGSHSLEHDSPTPRPSEACGBAQRLPSAPSGGAPIRDMGHHPQSGKOLPTGGHPG	712
Db	6956	LAPGSHSLEHDSPTPRPSEACGBAQRLPSAPSGGAPIRDMGHHPQSGKOLPTGGHPG	7015
QY	713	TAQPERPSPDPMQOPAPFCHPKQSGAPQEGCSPPHAPVAPCPGSPFPGSCKEAPLVPS	772
Db	7016	TAQPERPSPDPMQOPAPFCHPKQSGAPQEGCSPPHAPVAPCPGSPFPGSCKEAPLVPS	7075
QY	773	PFLGQAPPAKAPAKASPLDSKMGPDGILSGPRKPGCCSPGSAQASSQVSSLRVGS	832
Db	7076	PFLGQAPPAKAPAKASPLDSKMGPDGILSGPRKPGCCSPGSAQASSQVSSLRVGS	7135
QY	833	SOVGTPEGPSLDAEGWTOEADILSDSTPTLQRPQEQVMTWKPSLGGRGYAGVAGYGTFA	892
Db	7136	SOVGTPEGPSLDAEGWTOEADILSDSTPTLQRPQEQVMTWKPSLGGRGYAGVAGYGTFA	7195
QY	893	FGDAGGMLGGPFWABIIANVQSSEEEQEEARAESQSEEQEAEARASPLPQVSARVP	952
Db	7196	FGDAGGMLGGPFWABIIANVQSSEEEQEEARAESQSEEQEAEARASPLPQVSARVP	7255
QY	953	EYGRAFTRSSPEPTPWEDICQVSLVQIRDLSGDAEAAADTILSDISEVDPAYLNLSDLYDI	1012
Db	7256	EYGRAFTRSSPEPTPWEDICQVSLVQIRDLSGDAEAAADTILSDISEVDPAYLNLSDLYDI	7315
QY	1013	KYLPEEFMIPEKVPKSAQPPSPPMABEELABPEPTWMPGELPHAGLITTESEDDVD	1072
Db	7316	KYLPEEFMIPEKVPKSAQPPSPPMABEELABPEPTWMPGELPHAGLITTESEDDVD	7375
QY	1073	ALLAEAAVGRKRWKSSPSRSLFFHPQGRHULDEPAPBLGRURVKASVEHILSRILKGRPEG	1132
Db	7376	ALLAEAAVGRKRWKSSPSRSLFFHPQGRHULDEPAPBLGRURVKASVEHILSRILKGRPEG	7435

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RESULT 6
US-10-307-019-6
; Sequence 6, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
; APPLICANT: Zeng, Wenlin
; APPLICANT: Staton, Lawrence
; APPLICANT: SCIOS, INC
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
; FILE REFERENCE: SCIOS.021DVI
; CURRENT APPLICATION NUMBER: US/10/307,019
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/548,473
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/129,552
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2596
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-019-6

```

	Query Match	96.3%	Score 8417	DB 14	Length 2596
	Best Local Similarity	99.9%	Pred. No. 0	Mismatches	2
	Matches 1611	Conservative	0	Indels	0
	Gaps	0			
Qy	53	PPSMQVTTIEDVQAQTGGTAQFAALIEGPPQPSVTWKDSVOLVPSTRLSSQOQEGTTTSLV	112		
Db	984	PPSMQVTTIEDVQAQTGGTAQFAALIEGPPQPSVTWKDSVOLVPSTRLSSQOQEGTTTSLV	1043		
Qy	113	LRHVASKDAGVTTCLAQNTGGGVLCCKALLVLGDNEDPSKQSHRRKLHGFYEVKEIG	172		
Db	1044	LRHVASKDAGVTTCLAQNTGGGVLCCKALLVLGDNEDPSKQSHRRKLHGFYEVKEIG	1103		

QY 173 RGVFGVVRVQHGKNIKILCAAKFIPLRSRTAQAYRERDILAAALSHPLVTGLLDQFETRK 232
 Db 1104 RGVFGVVRVQHGKNIKILCAAKFIPLRSRTAQAYRERDILAAALSHPLVTGLLDQFETRK 1163
 QY 233 TLIIILELCSSEILLDLRLYRGVVTAEVKYIIOQLVEGLHYLHSHGVHLHDIKPSNIML 292
 Db 1164 TLIIILELCSSEILLDLRLYRGVVTAEVKYIIOQLVEGLHYLHSHGVHLHDIKPSNIML 1223
 QY 293 VHPAREDIKICDFGAQNIITAELOFQSGPEFVSPHIIQONPVSBASDIWANGVISYL 352
 Db 1224 VHPAREDIKICDFGAQNIITAELOFQSGPEFVSPHIIQONPVSBASDIWANGVISYL 1283
 QY 353 SLTCSPPFAGESDRATLNLVLEGRVSWSSPMAHLSEDAKFIKATLQAPQAPPSAAQC 412
 Db 1284 SLTCSPPFAGESDRATLNLVLEGRVSWSSPMAHLSEDAKFIKATLQAPQAPPSAAQC 1343
 QY 413 LSHPWFLKSMFAEEHFTNTQKFLFARSQWLSMSYKILVMSRSTPELIRGPPDPS 472
 Db 1344 LSHPWFLKSMFAEEHFTNTQKFLFARSQWLSMSYKILVMSRSTPELIRGPPDPS 1403
 QY 473 LGVAHLCRDYGGSSSSSSSSSDNELAPPARAKSLPPSPVTHSPLLHPRGFLRPSASLPEE 532
 Db 1404 LGVAHLCRDYGGSSSSSSSSSDNELAPPARAKSLPPSPVTHSPLLHPRGFLRPSASLPEE 1463
 QY 533 AEASERSTAPASPAGAPPAAGQCVPHSVIRSLFYHOAGHSPHGALAPGSRHP 592
 Db 1464 AEASERSTAPASPAGAPPAAGQCVPHSVIRSLFYHOAGHSPHGALAPGSRHP 1523
 QY 593 ARRRHLKGGYTAGALPGLRPLMHRVLEBAREEQATLLAKAPSPETALRLPASGTH 652
 Db 1524 ARRRHLKGGYTAGALPGLRPLMHRVLEBAREEQATLLAKAPSPETALRLPASGTH 1593
 QY 653 LAPGSHSLHSDSPSTPRPSSACGEAQLRSPAGGAPIRDMGHPQSGKOLPSTGGHPG 712
 Db 1594 LAPGSHSLHSDSPSTPRPSSACGEAQLRSPAGGAPIRDMGHPQSGKOLPSTGGHPG 1643
 QY 713 TAQPERSPDPSWGOPAPFCHPKQSAQOEGCSHPAVAPCPGSPGCKEAPLVPSS 772
 Db 1644 TAQPERSPDPSWGOPAPFCHPKQSAQOEGCSHPAVAPCPGSPGCKEAPLVPSS 1703
 QY 773 PFLGQFQAPPAPAKASPPLDKXMGPGDILSLGRPKPGPCSPGASQASSQVSSLRVGS 832
 Db 1704 PFLGQFQAPPAPAKASPPLDKXMGPGDILSLGRPKPGPCSPGASQASSQVSSLRVGS 1763
 QY 833 SQVGTPEGSLDAEGWTQAEPLDSPTLQRPQEQVTMRKFSLGGRGYAGVAGYGA 892
 Db 1764 SQVGTPEGSLDAEGWTQAEPLDSPTLQRPQEQVTMRKFSLGGRGYAGVAGYGA 1823
 QY 893 FGDAGGMLGQGPMMARIAWAVSQSEEEQEEARAESEEQEAPAESPLPQVSARVPV 952
 Db 1824 FGDAGGMLGQGPMMARIAWAVSQSEEEQEEARAESEEQEAPAESPLPQVSARVPV 1883
 QY 953 EVGRAPTRSPPTWEDIGQVSLQVIRDLSDGAEADTISLDISEVDPAYINLSLDYDI 1012
 Db 1884 EVGRAPTRSPPTWEDIGQVSLQVIRDLSDGAEADTISLDISEVDPAYINLSLDYDI 1943
 QY 1013 KYLPPEFMIKRVKPSAQOPEPPSPMAEELAEFPPTWPCGELGPHAGLEITESESDVD 1072
 Db 1944 KYLPPEFMIKRVKPSAQOPEPPSPMAEELAEFPPTWPCGELGPHAGLEITESESDVD 2003
 QY 1073 ALLAAVAVKRWKSSPSLSLFFHFGHPLPDEPAELGLRERVKASVEHISRLKGRPEG 1132
 Db 2004 ALLAAVAVKRWKSSPSLSLFFHFGHPLPDEPAELGLRERVKASVEHISRLKGRPEG 2063
 QY 1133 LEKEGPPKPKGLASPRISGLKSWDRAPTFLRSLDETIVLGQSVTLACOVSAQAQAT 1192
 Db 2064 LEKEGPPKPKGLASPRISGLKSWDRAPTFLRSLDETIVLGQSVTLACOVSAQAQAT 2123
 QY 1193 WSKDGAFLSSSRVLISATLKNFQLLTILVVAEDLGVTCTSVSNALGVTTTGVLRKAE 1252
 Db 2124 WSKDGAFLSSSRVLISATLKNFQLLTILVVAEDLGVTCTSVSNALGVTTTGVLRKAE 2183

QY 1253 RPSSSPCPDIBGVYADGVLLVWKPVESYGPVTYIVQCSLEGSSWTTLASDIFDCCYLTSK 1312
 Db 2184 RPSSSPCPDIBGVYADGVLLVWKPVESYGPVTYIVQCSLEGSSWTTLASDIFDCCYLTSK 2243
 QY 1313 LSRGGTYTERTACVSKAGMPYSSSEQVLLCGPSHLASEEESQGRSAQPLSTKTFAFQ 1372
 Db 2244 LSRGGTYTERTACVSKAGMPYSSSEQVLLCGPSHLASEEESQGRSAQPLSTKTFAFQ 2303
 QY 1373 TQIQGRFSPVVRQCKWEKASGRALAAKIIPYHPKDKTAVLREYALKGLRPHLAQHLHAAY 1432
 Db 2304 TQIQGRFSPVVRQCKWEKASGRALAAKIIPYHPKDKTAVLREYALKGLRPHLAQHLHAAY 2363
 QY 1433 LSPRHVLILELCSGPPELLPCLAEARASYSSEVKDYLMQMLSATOVLYHNOHILHLDLRS 1492
 Db 2364 LSPRHVLILELCSGPPELLPCLAEARASYSSEVKDYLMQMLSATOVLYHNOHILHLDLRS 2423
 QY 1493 NMIITEYNLLKVVLDLGNALQSLEKVLPSDKFKDYLETMAPELLEGQGVAVPQTDIWAIGV 1552
 Db 2424 NMIITEYNLLKVVLDLGNALQSLEKVLPSDKFKDYLETMAPELLEGQGVAVPQTDIWAIGV 2483
 QY 1553 TAPIMLSAEYPVSSSEGARDLQRLKGLVRLSRCVAGLSGGAVAFRLSTLCAQPMWRPCCA 1612
 Db 2484 TAPIMLSAEYPVSSSEGARDLQRLKGLVRLSRCVAGLSGGAVAFRLSTLCAQPMWRPCCA 2543
 QY 1613 SSCLOCPMLTEGPACSRDPAPVPTPTARLVRVVRNREKRRALLYKHNLAQVR 1665
 Db 2544 SSCLOCPMLTEGPACSRDPAPVPTPTARLVRVVRNREKRRALLYKHNLAQVR 2596
 RESULT 7
 US-10-182-243-46
 ; Sequence 46, Application US/10182243
 ; Publication No. US20040048310A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PLOWMAN, GREGORY D.
 ; APPLICANT: WHYTE, DAVID
 ; APPLICANT: MANNING, GERRARD
 ; APPLICANT: SUDARSANAM, SUCHA
 ; APPLICANT: MARTINEZ, RICARDO
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
 ; TITLE OF INVENTION: ENZYMES
 ; FILE REFERENCE: 038602/1366
 ; CURRENT APPLICATION NUMBER: US/10/182,243
 ; CURRENT FILING DATE: 2003-07-07
 ; PRIOR APPLICATION NUMBER: PCT/US01/02337
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 45
 ; LENGTH: 1618
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-182-243-46
 Query Match 96.1%; Score 8403; DB 12; Length 1618;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 161; Conservative 0; Mismatches 1; Indels 6; Gaps 1;
 QY 54 PSMQVTIEDVQAGTGGTAQFEAIEGDPQSPVWYKDSVLVDSTRLSQOQEGTYSVLV 113
 Db 1 PSMQVTIEDVQAGTGGTAQFEAIEGDPQSPVWYKDSVLVDSTRLSQOQEGTYSVLV 60
 QY 114 RHVASKDAGVYTCLAQNTGGVLCCKAELLVLG-----GDNEPDSEKSHRRKLHSFYEV 167
 Db 61 RHVASKDAGVYTCLAQNTGGVLCCKAELLVLGASHSLGDNEDSEKSHRRKLHSFYEV 120
 QY 168 KEEIGRGVFGVVRVQHGKNIKILCAAKFIPLRSRTAQAYRERDILAAALSHPLVTGLDQ 227
 Db 121 KEEIGRGVFGVVRVQHGKNIKILCAAKFIPLRSRTAQAYRERDILAAALSHPLVTGLDQ 180
 QY 228 FETKTKLILILELCSSEILLDLRLYRGVVTAEVKYIIOQLVEGLHYLHSHGVHLHDIKP 287
 Db 181 FETKTKLILILELCSSEILLDLRLYRGVVTAEVKYIIOQLVEGLHYLHSHGVHLHDIKP 240

QY 288 SNILMVHPAREDIKICDFGFAQNTIPAELOFQSYGSPFVSEIICQNPVSEASDIWANG 347
DB 241 SNILMVHPAREDIKICDFGFAQNTIPAELOFQSYGSPFVSEIICQNPVSEASDIWANG 300
QY 348 VISYLSLTCSSPAGSDRATLNLVLEGRVSWSSPMAHLSDEKDFIKATLQAPQARP 407
DB 301 VISYLSLTCSSPAGSDRATLNLVLEGRVSWSSPMAHLSDEKDFIKATLQAPQARP 360
QY 408 SAAQCLSHPWFLKSMFAEAEHFNITKQLFLARSRWORSLSMSYKSIILVMSRIPELLRGP 467
DB 361 SAAQCLSHPWFLKSMFAEAEHFNITKQLFLARSRWORSLSMSYKSIILVMSRIPELLRGP 420
QY 468 PDSPSLGVAPHLCRDTCGGSSSSSSSDNELAPARAKSLPPSPVTHSLHPRGFLRPSA 527
DB 421 PDSPSLGVAPHLCRDTCGGSSSSSSSDNELAPARAKSLPPSPVTHSLHPRGFLRPSA 480
QY 528 SLPEEAESRSTEAPAPASPEGAGPPAAQGCVRHRSVIRSLFYHQAGSEPEHGALAPG 587
DB 481 SLPEEAESRSTEAPAPASPEGAGPPAAQGCVRHRSVIRSLFYHQAGSEPEHGALAPG 540
QY 588 SRHPARRRHLLKGGYIAGALPOLREPLMEHRVLEBEAAREQATLLAKAPSFETALRLP 647
DB 541 SRHPARRRHLLKGGYIAGALPOLREPLMEHRVLEBEAAREQATLLAKAPSFETALRLP 600
QY 648 ASGTHLAPGSHSLHDSSTPRPSEACGEAQLRPLSAPSGAPIRDMGHQPGSKQLPST 707
DB 601 ASGTHLAPGSHSLHDSSTPRPSEACGEAQLRPLSAPSGAPIRDMGHQPGSKQLPST 660
QY 708 GHPTGAQPERPSPDSFWQAPAPFCHPKQGSAPQSGCPHPAVAPCPPGSPPPGSCKEAP 767
DB 661 GHPTGAQPERPSPDSFWQAPAPFCHPKQGSAPQSGCPHPAVAPCPPGSPPPGSCKEAP 720
QY 768 LVPSSPFLGQOPAPPAPAKASPLDLSKMGPGDISLPGRPKPCPCSSPGSASQASSSQVSS 827
DB 721 LVPSSPFLGQOPAPPAPAKASPLDLSKMGPGDISLPGRPKPCPCSSPGSASQASSSQVSS 780
QY 828 LRVSSQVGTQEPGSLDAGWTOEABDLSDSPTTLQROEQVTKRKFSLGGRGYAGVAG 887
DB 781 LRVSSQVGTQEPGSLDAGWTOEABDLSDSPTTLQROEQVTKRKFSLGGRGYAGVAG 840
QY 888 YGTFAFGGAGMLGQCPMWARIAWAVSQSEEEQEAARASQSEEQEAARASPLPQVS 947
DB 841 YGTFAFGGAGMLGQCPMWARIAWAVSQSEEEQEAARASQSEEQEAARASPLPQVS 900
QY 948 ARVPVEVGRAPTRSSPEPTPWEDIGQVSLVQIRDLSDGAEAAADTISLDSIVDPAYLNL 1007
DB 901 ARVPVEVGRAPTRSSPEPTPWEDIGQVSLVQIRDLSDGAEAAADTISLDSIVDPAYLNL 960
QY 1008 DLYDIKYLPEFMIFRKVPKSAQPPSPMAEELAEPEPTWMPGELGPHAGLEITEE 1067
DB 961 DLYDIKYLPEFMIFRKVPKSAQPPSPMAEELAEPEPTWMPGELGPHAGLEITEE 1020
QY 1068 SEDVDALLAEAAVGRKRWSSPSRSLFHPGPHLPLDEPAELGLRERKASVEHISILK 1127
DB 1021 SEDVDALLAEAAVGRKRWSSPSRSLFHPGPHLPLDEPAELGLRERKASVEHISILK 1080
QY 1128 GRPEGLEKSGPPRKKPGLASFLSLGKSWDRAPTFLRELSDETIVVLGQSVTLACQVSAQP 1187
DB 1081 GRPEGLEKSGPPRKKPGLASFLSLGKSWDRAPTFLRELSDETIVVLGQSVTLACQVSAQP 1140
QY 1188 AQAATWSKQAPLESSESRVLIISATLKNFOLLTLVVVAEDLGVTVCVSNALGVTTTGV 1247
DB 1141 AQAATWSKQAPLESSESRVLIISATLKNFOLLTLVVVAEDLGVTVCVSNALGVTTTGV 1200
QY 1248 LRKAERPPSSPCPDIGEVYADGVLLVWKFVSEYGPVTIVQCSLEGGSWTTLASDIFDCC 1307
DB 1201 LRKAERPPSSPCPDIGEVYADGVLLVWKFVSEYGPVTIVQCSLEGGSWTTLASDIFDCC 1260
QY 1308 YLTSKLSRGTTYTFRFACVSKAGMGYPSPSPSEOVLLGGPSHLASEESQGSAPLPSTK 1367
DB 1261 YLTSKLSRGTTYTFRFACVSKAGMGYPSPSEOVLLGGPSHLASEESQGSAPLPSTK 1320

QY 1368 TFAFOTQORGFSSVVRQWCKASGRALAAKIIIPHPKDKTAVLREYEALGLRPHLAQ 1427
DB 1321 TFAFOTQORGFSSVVRQWCKASGRALAAKIIIPHPKDKTAVLREYEALGLRPHLAQ 1380
QY 1428 LHAAYLSRPHLVLIILELCSGPPELLPCLAEASYSSESEVKDYLMQWLSATOYLHNOHILHL 1487
DB 1381 LHAAYLSRPHLVLIILELCSGPPELLPCLAEASYSSESEVKDYLMQWLSATOYLHNOHILHL 1440
QY 1488 DURSENMIITEYNLLKVVVDLGNQAQSLSOEKLPSDKFDYLETWAPELLEGGGAVPQTDI 1547
DB 1441 DURSENMIITEYNLLKVVVDLGNQAQSLSOEKLPSDKFDYLETWAPELLEGGGAVPQTDI 1500
QY 1548 WAIGVTAFTMLSAEYFVSSEGGARDLQRLKGLVRLSCYAGLSGGGAVAFURSTLCQAPW 1607
DB 1501 WAIGVTAFTMLSAEYFVSSEGGARDLQRLKGLVRLSCYAGLSGGGAVAFURSTLCQAPW 1560
QY 1608 GRPCASSCLQCPWLTBEGPACSRPAPVTFTPARLVFVRNREKRALLYKXHNLAQVR 1665
DB 1561 GRPCASSCLQCPWLTBEGPACSRPAPVTFTPARLVFVRNREKRALLYKXHNLAQVR 1618

RESULT 8
US-10-307-019-4
; Sequence 4, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
; APPLICANT: Zeng Wenlin
; APPLICANT: Stanton, Lawrence
; APPLICANT: Sciots, Inc.
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
; FILE REFERENCE: SCIOS-021DVL
; CURRENT APPLICATION NUMBER: US/10/307,019
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/548,473
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/129,552
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1610
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-019-4

Query Match 96.1%; Score 8399; DB 14; Length 1610;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 56 MQVTIEDVQAOTGGTGAQPEALIEGDPQPSVTWYKDSVOLVDSTRLSQOQEGTTYSLVRH 115
DB 1 MQVTIEDVQAOTGGTGAQPEALIEGDPQPSVTWYKDSVOLVDSTRLSQOQEGTTYSLVRH 60
QY 116 VASKDAGVYTCLAQNTGGQVLCKAELLVLGSDNEPDSEKSHRKLHSFYEVKEEIGRGV 175
DB 61 VASKDAGVYTCLAQNTGGQVLCKAELLVLGSDNEPDSEKSHRKLHSFYEVKEEIGRGV 120
QY 176 FGFVKRVQHKGNKILCAAKFIPLRSTRQAAYRERDILAALSHPLVTGLDQFETKTLI 235
DB 121 FGFVKRVQHKGNKILCAAKFIPLRSTRQAAYRERDILAALSHPLVTGLDQFETKTLI 180
QY 236 LLELCSSFEELDLRYKGVVTEAEVKVYIQQLVGSHVHLHSHVGLHLDIKPSNLMVHP 295
DB 181 LLELCSSFEELDLRYKGVVTEAEVKVYIQQLVGSHVHLHSHVGLHLDIKPSNLMVHP 240
QY 296 AREDIKICDFGFAQNTIPAELOFQSYGSPFVSEIICQNPVSEASDIWANGVISYLSLT 355
DB 241 AREDIKICDFGFAQNTIPAELOFQSYGSPFVSEIICQNPVSEASDIWANGVISYLSLT 300
QY 356 CSSPAGESDRATLNLVLEGRVSWSSPMAHLSDEKDFIKATLQAPQARPSPAAQCLSH 415
DB 301 CSSPAGESDRATLNLVLEGRVSWSSPMAHLSDEKDFIKATLQAPQARPSPAAQCLSH 360

1441	ITEYNLLKVVDLGNAGLSQEKVLPSDRFKDYLETWAPELLGGQAVPQTDIWAIGTAF	1500
1556	IMLSABYPVSSGARDQLGRLGKGLVRSRCYAGLSGGGAVAFILRSTLCQAPWGRPCASSC	1615
1501	IMLSABYPVSSGARDQLGRLGKGLVRLSRCYAGLSGGGAVAFILRSTLCQAPWGRPCASSC	1560
1616	LOCPWLTESGPACSRPAPVTFPTARLVRVVRNREKERRALLYKRNLAQVR	1665
1561	LOCPWLTESGPACSRPAPVTFPTARLVRVVRNREKERRALLYKRNLAQVR	1610

US-10-307-019-1
; Sequence 1, Application US/10307019
; Publication No: US20030108533A1

Query Match	80.9%	Score 7069;	DB 14;	Length 1351;
Best Local Similarity	99.9%	Pred. No. 0;		
Conservative	1149	Mismatches 1;	Indels 0;	Gaps 0;

Query Match 80.9%; Score 7069; DB 14; Length 1351;

QY 316 LQFSQYGSBFBVSPELIIQQNPVSEASDIWAMGVISYLSITCSPSPAGESDRATLLNVLEG 375

QY	376	RVSSSPMAHLSEDAKFIKATLQRAPOARPSAAQCISHPWFLKSMPEAEAHFINTKQL	435
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QY 436 KFLIARSRWORSMLSYKSIILVNRSIPELLRGPDPSPGLAVRHLCRDTCGSSSSSSSSSDN 495

QY 496 ELAPPARAKI PPPSPVTHPSLLHPRGFLRPSALPEERAEASERSTEAPAPASPEGAGPP 555

QY 556 AAQGVPRHSVIRSLFYHQAGSPESHGALPGSRRHPPARRRHLLKGGYIAGALPGUREPL 615

QY 616 MEHRVLEBBAAREEQATLLAKAPSFETALRLPASGTHLAPGHSIHEDSDSPSTPRPSEA 675

QY 676 CGEAOQLPSAPSGGAPTRDMGHGHPQGSKOLPSTGGHPTGTQPERPSPDPSWGCOPAPFCHPK 735

QY	736	QGSAPQEGCSPHPAVAPCPPGSPFP	QGSKEAPLVSSPFLGQPPAPAKASPLDSKM	795
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Qy 796 GPGDISLPGRPKPGPCSSPGSASQASSQVSSLRVGSSQVGTETPGPSLDAGWTOEADL 855

482 GPGDISLPGKPGKPGSCPSGASQSSQVSSLRVGSQVGTPEGSLDAGWTQEAEDL 541
QY 856 SDSTPTLQRPQOQVTKRKSLSGRGAGYAGVGTGTFAGDAGGMLGQGPMMARIAMAVS 915
Db 542 SDSTPTLQRPQOQVTKRKSLSGRGAGYAGVGTGTFAGDAGGMLGQGPMMARIAMAVS 601
QY 916 QSEEEQEEARASQSEEEQEEARASPLQVSGARPVEVGRAPTRSSPEPTPWEDIGQVS 975
Db 602 QSEEEQEEARASQSEEEQEEARASPLQVSGARPVEVGRAPTRSSPEPTPWEDIGQVS 661
QY 976 LVQIRDLSDGABAAADTISLDSIVDPAYLNLSDLYDKYLPPEFMIFRKVPKSAQPEPPS 1035
Db 662 LVQIRDLSDGABAAADTISLDSIVDPAYLNLSDLYDKYLPPEFMIFRKVPKSAQPEPPS 721
QY 1036 PMAEELAEPEPTWMPGELGPHAGLEITESESDVALLAAVGRKRWSSPSRSLFH 1095
Db 722 PMAEELAEPEPTWMPGELGPHAGLEITESESDVALLAAVGRKRWSSPSRSLFH 781
QY 1096 FPGRHPLDPAELGLRERVKASVEHISRLKRGPEGLKEGPPKPKGLASFRLSGLKS 1155
Db 782 FPGRHPLDPAELGLRERVKASVEHISRLKRGPEGLKEGPPKPKGLASFRLSGLKS 841
QY 1156 WDRAPFLRLSDTETVVLGOSVTLAQVSAQAAQATWSKCAPLESSRVLISATLKNF 1215
Db 842 WDRAPFLRLSDTETVVLGOSVTLAQVSAQAAQATWSKCAPLESSRVLISATLKNF 901
QY 1216 QLLTILVVAEDLGVYTCVSNALGVTGTVLKAERPSSSPCPDICEVYADGVLLVWK 1275
Db 902 QLLTILVVAEDLGVYTCVSNALGVTGTVLKAERPSSSPCPDICEVYADGVLLVWK 961
QY 1276 FVBSYGPVTYIVQCSLEGGSWTTLASDIFDCCYLTSKLSRGTYTFTACVSKAGMGFYS 1335
Db 962 FVBSYGPVTYIVQCSLEGGSWTTLASDIFDCCYLTSKLSRGTYTFTACVSKAGMGFYS 1021
QY 1336 SPSEOVLLGSPSHLASEESQGRSAPLSTKTFTAFQTOIQGRFSVVRQWCKASGRAL 1395
Db 1022 SPSEOVLLGSPSHLASEESQGRSAPLSTKTFTAFQTOIQGRFSVVRQWCKASGRAL 1081
QY 1396 AAKIIPYHPKDKTAVLREYALKGLRPHLAQLHAAYLSPRHLVILELCSGPELLPCLA 1455
Db 1082 AAKIIPYHPKDKTAVLREYALKGLRPHLAQLHAAYLSPRHLVILELCSGPELLPCLA 1141
QY 1456 ERASYSESEVKDYLWMLSATQVYLNHNOHILHDLSENMIITEYNLLKVVLDLNAQSLSQ 1515
Db 1142 ERASYSESEVKDYLWMLSATQVYLNHNOHILHDLSENMIITEYNLLKVVLDLNAQSLSQ 1201
QY 1516 EKVLPDKFKDYLETWAPLELGGGAVPQTDIWAIGVTAFIMLSAEYFVSSEGARDLQRG 1575
Db 1202 EKVLPDKFKDYLETWAPLELGGGAVPQTDIWAIGVTAFIMLSAEYFVSSEGARDLQRG 1261
QY 1576 LRKGLVRLSCYAGLSGGAVALRSTLCAQPKRCPACSSCLOCPLWTEEGPACSRPAPVT 1635
Db 1262 LRKGLVRLSCYAGLSGGAVALRSTLCAQPKRCPACSSCLOCPLWTEEGPACSRPAPVT 1321
QY 1636 FPTARLRFVVRNREKRRALLYKEHNLAQVR 1665
Db 1322 FPTARLRFVVRNREKRRALLYKEHNLAQVR 1351

RESULT 10
US-10-311-034-20
; Sequence 20, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.

APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: CHAMLA, Narinder K.
APPLICANT: YAO, Monique G.
APPLICANT: LU, Dyung Aina M.
APPLICANT: GREENWALD, Sara R.
APPLICANT: RAMKUMAR, Jayalakmi
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: KEARNEY, Liam
APPLICANT: BURFORD, Neil
APPLICANT: NGUYEN, Daniel B.
APPLICANT: TANG, Y. Iom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HE, Ann
APPLICANT: THORNTON, Michael
APPLICANT: HAFALIA, April
APPLICANT: ARVIZU, Chandra S.
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: LO, Terence P.
APPLICANT: KHAN, Farrah A.
APPLICANT: RECIPON, Shirley A.
APPLICANT: AZIMZAI, Yalda
APPLICANT: POLICKY, Jennifer L.
APPLICANT: DING, Li
APPLICANT: GREYHER, Megan
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; 60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-15
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 20
LENGTH: 871
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040023242A1 3016969CD1
US-10-311-034-20

Query Match 51.9%; Score 4533; DB 16; Length 871;
Best Local Similarity 100.0%; Pred. No. 1.9e-218;
Matches 871; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 795 MGPGDISLPGKPGKPGSCPSGASQSSQVSSLRVGSQVGTPEGSLDAGWTQEAED 854
Db 1 MGPGDISLPGKPGKPGSCPSGASQSSQVSSLRVGSQVGTPEGSLDAGWTQEAED 60
QY 855 LSDSTPTLQRPQOQVTKRKSLSGRGAGYAGVGTGTFAGDAGGMLGQGPMMARIAMAV 914
Db 61 LSDSTPTLQRPQOQVTKRKSLSGRGAGYAGVGTGTFAGDAGGMLGQGPMMARIAMAV 120
QY 915 QSEEEQEEARASQSEEEQEEARASPLQVSGARPVEVGRAPTRSSPEPTPWEDIGQV 974
Db 121 QSEEEQEEARASQSEEEQEEARASPLQVSGARPVEVGRAPTRSSPEPTPWEDIGQV 180
QY 975 SLVQIRDLSDGABAAADTISLDSIVDPAYLNLSDLYDKYLPPEFMIFRKVPKSAQPEPP 1034
Db 181 SLVQIRDLSDGABAAADTISLDSIVDPAYLNLSDLYDKYLPPEFMIFRKVPKSAQPEPP 240
QY 1035 SPMAEELAEPEPTWMPGELGPHAGLEITESESDVALLAAVGRKRWSSPSRSLF 1094
Db 241 SPMAEELAEPEPTWMPGELGPHAGLEITESESDVALLAAVGRKRWSSPSRSLF 300
QY 1095 HPPGSHLPLDPAELGLRERVKASVEHISRLKRGPEGLKEGPPKPKGLASFRLSGLK 1154

Db 301 HFGRLPLDEPAELGLRERVKASVEHISRLKGRPEGLKEGPPKPKGLASFLSLGLK 360
Qy 1155 SWDRAPTFRLBELSDETVLQGSVTLACQVSAQPAQAATWSKDGAPLESRRVLISATLKN 1214
Db 361 SWDRAPTFRLBELSDETVLQGSVTLACQVSAQPAQAATWSKDGAPLESRRVLISATLKN 420
Qy 1215 FQLLTILVVAEDLGVYTCVSVALGTVTGVLKKAERPSSPCPDIGEYVADGVLLVM 1274
Db 421 FQLLTILVVAEDLGVYTCVSVALGTVTGVLKKAERPSSPCPDIGEYVADGVLLVM 480
Qy 1275 KPVSIGPVYIYVQCSLGGSWTTLASDIFDCCYLTSKLSRGTYTFTACVSKAGMGPY 1334
Db 481 KPVSIGPVYIYVQCSLGGSWTTLASDIFDCCYLTSKLSRGTYTFTACVSKAGMGPY 540
Qy 1335 SSPSEQVLLGGPSHLASEESQGRSAQPLPSTKTFQIQGRFVSVRQCEKASGRA 1394
Db 541 SSPSEQVLLGGPSHLASEESQGRSAQPLPSTKTFQIQGRFVSVRQCEKASGRA 600
Qy 1395 LAAKIIPYHPKDKTAVLREYALKGRHPLAQLHAAYLSRHLVLIILELCSGPELLPCL 1454
Db 601 LAAKIIPYHPKDKTAVLREYALKGRHPLAQLHAAYLSRHLVLIILELCSGPELLPCL 660
Qy 1455 AERASYSSEVKDYLQWMLSATQYLHNOHILHLDLRSENMIITEYNLLKVVLDLGNASLS 1514
Db 661 AERASYSSEVKDYLQWMLSATQYLHNOHILHLDLRSENMIITEYNLLKVVLDLGNASLS 720
Qy 1515 QEKVLPDSKDKYLETMAPELLEGQAVPQTDIWAIGVTAFTIMLSAEYVPSSEGARDLQ 1574
Db 721 QEKVLPDSKDKYLETMAPELLEGQAVPQTDIWAIGVTAFTIMLSAEYVPSSEGARDLQ 780
Qy 1575 GLRKGVLRLSRVYAGLSGAVAFRLSTLCAQPWGRPCASSCCLQCPWLTTEGPACSRPAPV 1634
Db 781 GLRKGVLRLSRVYAGLSGAVAFRLSTLCAQPWGRPCASSCCLQCPWLTTEGPACSRPAPV 840
Qy 1635 TPTARLVRVVRNREKRALLYKRNHLAQVR 1665
Db 841 TPTARLVRVVRNREKRALLYKRNHLAQVR 871

RESULT 11

US-10-307-019-7

; Sequence 7, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
; APPLICANT: Zeng, Wenlin
; APPLICANT: Stanton, Lawrence
; APPLICANT: SCIOS, INC.
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
; FILE REFERENCE: SCIOS.021DV1
; CURRENT APPLICATION NUMBER: US/10/307,019
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/548,473
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/129,552
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-019-7

Query Match 51.8%; Score 4529; DB 14; Length 871;
Best Local Similarity 99.9%; Pred. No. 2.9e-218;
Matches 870; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 795 MFGEDISLGRPKPGPCSSPGASQSSQVSLRVGSSQVGTETPGPSLDAEGWTQAEAD 854
Db 1 MFGEDISLGRPKPGPCSSPGASQSSQVSLRVGSSQVGTETPGPSLDAEGWTQAEAD 60
Qy 855 LSDSTPTLQRPQVTRKFSLGGRGYAGVAGYGTAFGGDAGGMLGQGPWARIWAW 914

Db 61 LSDSTPTLQRPQVTRKFSLGGRGYAGVAGYGTAFGGDAGGMLGQGPWARIWAW 120
Qy 915 SOSSEEQBEARAEASQSEEQBARAEPLQVARSAPVPEVGRAPTRSPPTWEDICQV 974
Db 121 SOSSEEQBEARAEASQSEEQBARAEPLQVARSAPVPEVGRAPTRSPPTWEDICQV 180
Qy 975 SLVQIRDLSDGDAADTSLDISVDPAVLNLSLDYDIKYLPPFEFMIIFRKYPKSAQPPPP 1034
Db 181 SLVQIRDLSDGDAADTSLDISVDPAVLNLSLDYDIKYLPPFEFMIIFRKYPKSAQPPPP 240
Qy 1035 SPMAEELAEFPPEPTWMPGELGPHAGLEITESESDVDALLAEAAVGRKRWSSPSRSLF 1094
Db 241 SPMAEELAEFPPEPTWMPGELGPHAGLEITESESDVDALLAEAAVGRKRWSSPSRSLF 300
Qy 1095 HPPGRHLPLDEPAELGLRERVKASVEHISRLKGRPEGLKEGPPKPKGLASFLSLGLK 1154
Db 301 HPPGRHLPLDEPAELGLRERVKASVEHISRLKGRPEGLKEGPPKPKGLASFLSLGLK 360
Qy 1155 SWDRAPTFRLBELSDETVLQGSVTLACQVSAQPAQAATWSKDGAPLESRRVLISATLKN 1214
Db 361 SWDRAPTFRLBELSDETVLQGSVTLACQVSAQPAQAATWSKDGAPLESRRVLISATLKN 420
Qy 1215 FQLLTILVVAEDLGVYTCVSVALGTVTGVLKKAERPSSPCPDIGEYVADGVLLVM 1274
Db 421 FQLLTILVVAEDLGVYTCVSVALGTVTGVLKKAERPSSPCPDIGEYVADGVLLVM 480
Qy 1275 KPVSIGPVYIYVQCSLGGSWTTLASDIFDCCYLTSKLSRGTYTFTACVSKAGMGPY 1334
Db 481 KPVSIGPVYIYVQCSLGGSWTTLASDIFDCCYLTSKLSRGTYTFTACVSKAGMGPY 540
Qy 1335 SSPSEQVLLGGPSHLASEESQGRSAQPLPSTKTFQIQGRFVSVRQCEKASGRA 1394
Db 541 SSPSEQVLLGGPSHLASEESQGRSAQPLPSTKTFQIQGRFVSVRQCEKASGRA 600
Qy 1395 LAAKIIPYHPKDKTAVLREYALKGRHPLAQLHAAYLSRHLVLIILELCSGPELLPCL 1454
Db 601 LAAKIIPYHPKDKTAVLREYALKGRHPLAQLHAAYLSRHLVLIILELCSGPELLPCL 660
Qy 1455 AERASYSSEVKDYLQWMLSATQYLHNOHILHLDLRSENMIITEYNLLKVVLDLGNASLS 1514
Db 661 AERASYSSEVKDYLQWMLSATQYLHNOHILHLDLRSENMIITEYNLLKVVLDLGNASLS 720
Qy 1515 QEKVLPDSKDKYLETMAPELLEGQAVPQTDIWAIGVTAFTIMLSAEYVPSSEGARDLQ 1574
Db 721 QEKVLPDSKDKYLETMAPELLEGQAVPQTDIWAIGVTAFTIMLSAEYVPSSEGARDLQ 780
Qy 1575 GLRKGVLRLSRVYAGLSGAVAFRLSTLCAQPWGRPCASSCCLQCPWLTTEGPACSRPAPV 1634
Db 781 GLRKGVLRLSRVYAGLSGAVAFRLSTLCAQPWGRPCASSCCLQCPWLTTEGPACSRPAPV 840
Qy 1635 TPTARLVRVVRNREKRALLYKRNHLAQVR 1665
Db 841 TPTARLVRVVRNREKRALLYKRNHLAQVR 871

RESULT 12

US-10-307-019-8

; Sequence 8, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
; APPLICANT: Zeng, Wenlin
; APPLICANT: Stanton, Lawrence
; APPLICANT: SCIOS, INC.
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
; FILE REFERENCE: SCIOS.021DV1
; CURRENT APPLICATION NUMBER: US/10/307,019
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/548,473
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/129,552
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0

US-10-307-019-8

Query Match 28.0%; Score 2447.5; DB 14; Length 548;
Best Local Similarity 86.4%; Pred. No. 2.1e-114;
Matches 472; Conservative 27; Mismatches 46; Indels 1; Gaps 1;

US-10-307-019-8

Query Match 28.0%; Score 2447.5; DB 14; Length 548;
Best Local Similarity 86.4%; Pred. No. 2.1e-114;
Matches 472; Conservative 27; Mismatches 46; Indels 1; Gaps 1;

US-10-307-019-9

Query Match 27.6%; Score 2415.5; DB 14; Length 548;
Best Local Similarity 85.7%; Pred. No. 8.2e-113;
Matches 468; Conservative 25; Mismatches 52; Indels 1; Gaps 1;

US-10-307-019-9

Query Match 27.6%; Score 2415.5; DB 14; Length 548;
Best Local Similarity 85.7%; Pred. No. 8.2e-113;
Matches 468; Conservative 25; Mismatches 52; Indels 1; Gaps 1;

US-10-425-114-37530

Sequence 37530, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)E
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4119-136-D3_FLI.pdp
US-10-425-114-37530

Query Match 23.4%; Score 2045; DB 12; Length 390;

US-10-425-114-37530

Sequence 37530, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)E
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4119-136-D3_FLI.pdp
US-10-425-114-37530

Query Match 23.4%; Score 2045; DB 12; Length 390;

US-10-425-114-37530

Sequence 37530, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)E
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4119-136-D3_FLI.pdp
US-10-425-114-37530

Query Match 23.4%; Score 2045; DB 12; Length 390;

US-10-425-114-37530

Sequence 37530, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)E
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4119-136-D3_FLI.pdp
US-10-425-114-37530

Query Match 23.4%; Score 2045; DB 12; Length 390;

Best Local Similarity 100.0%; Pred. No. 1.8e-94;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1276 PVESYGPVTYIVQCSLEGGSWTTLASDIFDCCYLTSKLSRGTTTFRACVSKAGMGPYS 1335
Db 1 PVESYGPVTYIVQCSLEGGSWTTLASDIFDCCYLTSKLSRGTTTFRACVSKAGMGPYS 60
QY 1336 SPSEVILGGPSHLASEESQGRSAQPLPSTKTFATQIQGRFVSVRQCKEASGRAL 1395
Db 61 SPSEVILGGPSHLASEESQGRSAQPLPSTKTFATQIQGRFVSVRQCKEASGRAL 120
QY 1396 AAKIIPYHPKDTAVLREYALKGRHPHLAQHAAYLSPHLVILLELCSGPPELLPCLA 1455
Db 121 AAKIIPYHPKDTAVLREYALKGRHPHLAQHAAYLSPHLVILLELCSGPPELLPCLA 180
QY 1456 ERASVSESEVKYQMLSATQYLNHILHDLRSENMIITEYNLLKVDLGNASLSQ 1515
Db 181 ERASVSESEVKYQMLSATQYLNHILHDLRSENMIITEYNLLKVDLGNASLSQ 240
QY 1516 EKVLPDSDFKDYLETWAPELLEGGQAVPQTDIWAIGTAFMLSAEYVPSSEGARDLQRG 1575
Db 241 EKVLPDSDFKDYLETWAPELLEGGQAVPQTDIWAIGTAFMLSAEYVPSSEGARDLQRG 300
QY 1576 LRKGLVRLSRVAGLSGGAVAFRLSTLCAQPNRGPCASSCLOCPWLTEEGPACSRPAPVT 1635
Db 301 LRKGLVRLSRVAGLSGGAVAFRLSTLCAQPNRGPCASSCLOCPWLTEEGPACSRPAPVT 360
QY 1636 FTAIRLVFVRNREKRALLYKRNLAQVR 1665
Db 361 FTAIRLVFVRNREKRALLYKRNLAQVR 390

RESULT 15

US-10-333-314-18
; Sequence 18, Application US/10333314
; Publication No. US20030211093A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
; APPLICANT: HAFALIA, April J.A.; CHAWLA, Nandinder K.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.
; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAL, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0162 USN
; CURRENT APPLICATION NUMBER: US/10/333,314
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: PCT/US01/23092
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,038
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/222,112
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,831
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,729
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 2380
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7477141CD1
US-10-333-314-18

Query Match 22.6%; Score 1973; DB 12; Length 2380;
Best Local Similarity 29.3%; Pred. No. 6.4e-90;
Matches 568; Conservative 236; Mismatches 638; Indels 498; Gaps 50;
QY 54 PSMQVITDVQAGTGAQFAEIIIEGDPQSVTVYKDSVOLVDSTRLSQOQEGTTVSLVL 113
Db 598 PPSIMEDVEVGAGTARFVAVVEGKPLFDIMWYKDEVLTTESHSVSVFYENECSLVV 657
QY 114 RHVASDAGVYTCIAQNTGQVLCKAELVLGSDN---EPDSEKQSHR-RKLHSEYEVK 168
Db 658 LSTGAQGGVYTTCTAQLAGEVSCKAELAVHSAQTAAMEVEGVEDDHGRRLSDFYDIH 717
QY 169 EIEGRGVFGVFKRVQHKMKILCAAKFIPLRSTRAQAYRERDILAALSHPLVTGLDQF 228
Db 718 QEIGRGAFSYLRIRIVERSGGLFEAFKFIPOAKPKASARREARLLARLOCHDCVLYPHEAF 777
QY 229 ETRKTLILILELCSSELDRLRYKGVVTEAEVKVYIQQLVEGLHYLHSHGVHLHDKPS 288
Db 778 ERRRGVIVITVTELC-TEELLERJARKPTVCESEIRAYMRQVLEGIHYLHSHGVHLHDKPE 836
QY 289 NILMVHPA--REDIKICDFGFAQNIITPAELQFSQSGSPFVSPETIQONPVSEASDIWAM 346
Db 837 NLLVMDGAAGEQQVRCIDFGNAQELTFGBPQYCOYGTPEFVAPEIVNQSPVSGVTDIWPV 896
QY 347 GVISYLSLTCSSPAGESDRATLLNVLEGRVSNSSPMAHLSSEDAKDF-IKATLQAPQA 405
Db 897 GVVAFLCTGISPFVGENDRITLLMNRNVNVAPEETFLSLREARGFLIKVLVQ--DRL 954
QY 406 RPSAAOCLSHPWELKMPABEAHFINTKQLKFLARSRWQSRMSYKSLVWMSIPELLR 465
Db 955 RPTAETLEHPWFKTOAKGAB---VSTDHLKFLSRRRWQSRQISYKCHLVLPPELLR 1011
QY 466 GPPDSPSLGVARHLCRDITGGSSSSSSSSDNEL-----APFARAK-SLPPSPVTH 513
Db 1012 APPERVVMTFRR-PPPSGGLSSSDSEEELEELPSVPRPQLOPFGSGRVSITDPTED 1070
QY 514 SPILHPRGFLRPSASLPEAEASERSTEAPAPASPEGAGPAAQGVPRHVSIR----- 568
Db 1071 EALGTETGATPMDWQEGQRAQSPQOEAPSPALPSPQOEPA--GASPRGELRGSSA 1129
QY 569 -----SLFVHQAG--ESPHEGALAPG-----SRHPARRHLLK 600
Db 1130 ESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEGEYAOQLRQLRLR 1189
QY 601 GGYIAGALPGLREPLMEH-----RVLEEEAAREEQATL---LAKAPSFETALR 645
Db 1190 GGPEDGVSLRGLRPLLESIGGRARDPRMAASSEAPHPQPPLENRGLQKSSFSQGEA 1249
QY 646 LPASGTHLAFGHSHLSHDSPTPR-----PSSACGEAQRLPSAGPGAPIRMHGHQGS 701
Db 1250 EP-RGRHRRAGAPLEIPVARLGARLQESPSLSALSEAQ--PSSPA-----RPSAP 1297
QY 702 KQLPSTGGHPTAQPERPSPDSEWQOPAPFCHPKQGSAPQEGCSHPAVAPCPGPGFPFG 761
Db 1298 K--PST---PKSAEPSSATTPSDAPQPPAP--QPAQKAPEPREPVRASKEAP-----PPQ 1346
QY 762 SCK--EAPLVPSPPFLGQ-----POAPPAPAK-----ASPPLDSKMG 797
Db 1347 ALQTLALPLTFYAIQISLQLSCHAQPSQGPAPAPSEPKPHAARVAVASPP----- 1399
QY 798 GDISLPGRPKPGPCSPGASQSSQVSLRVGSGVGTGTPGSPSLDAEGWTOEAEPLSD 857
Db 1400 -----PGAEKRVPSAGGPPVLAEKARVPT-----VPPRPGSSSSSSTENLESEAVFE 1447
QY 858 STPTLQSPQEQVMTWRKFSLGGRGYAGVAGYGTAFAGDAGGMLGQGPWWARIANAVSQS 917
Db 1448 A--KFKSRRES-----PLSLGLR-----LLSRS 1468

918	EEEQEEAR-ABSQSEBQEQEARAESPLPQVVSARPVEVGRAPTRSSPEPTFWEDICQVSL	976
1469	RSEGRFPGRGAEEDGTRSPAGTFL-ELVRRPESR-----	1505
977	VOIRDL\$-GDAAEADTISIDISEVDPVAVLNLSLYIKYLPFFBPMIFRKVPKSAQPEPP	1034
1506	-SVQDLRAVGEPLVRELSLSQ-----RLRTPPAQR-----	1538
1035	SPMAEELABPEPTWPPGELPHAGLBITESESDVALLAAVAGRKRW-----	1086
1539	-----HPAEARGDGG-----ESSEGG\$ARGSPVLAMRRRLSPTLERLS	1578
1087	-----SGPSRSLPHFPGRHLPLDEPAELGLRERVKASVEHISRLIKGRP-----	1130
1579	SRLQESGSSD\$GASGR\$TFL-----FGRLRAT\$EGESLRRL--GUPHNQLAAQAGAT	1631
1131	-----EGLEKEGP-----PKKPGKLASFRLSG-----LK	1154
1632	TP\$AESLGS\$ASAT\$GSSAPGESRSRLWGRPRKDKGL\$PPNLSASVOEELGHQTVRS	1691
1155	SWDRAPFLRELSDET\$VVLQ\$VTLACQVSAQAAQATMSKDGAPL\$SSSRVLISATLKN	1214
1692	ESDPPFVFIKLDQVLLGE\$ATLCLCPA\$PAHISW\$KDKSL\$B\$ESV\$II\$V\$CKDG	1751
1215	FOLITLIVVAELGVTVCSV\$NALGT\$TTGVLRKAER\$PSS\$PCPDIGEVYADGVLLW	1274
1752	QOLLSIPRAGKRHAGLYECSAT\$VNLG\$IT\$SSCTVAVARVPGKLAPPEVQTYODTALVW	1811
1275	KPV\$SYG\$VTVI\$VOC\$LEGG\$-WTLIASDIPCCVLT\$KLSRG\$GTYITFRACV\$SKAGMP	1333
1812	KPG\$DRAPCTYTLERRVDG\$SVH\$PVSSGI\$PCYTYN\$THLPVGVTVF\$FVACN\$RAGQG	1871
1334	YSSP\$EQVLLGG-----	1345
1872	FSN\$SEKVFVRGTQD\$SAVPSAAHQ\$BAPVTSRPARAPD\$PTSLAPPLA\$PAAPT\$P\$SVT	1931
1346	-----PSHLASEESOG-----BSAOP-LPST-----	1366
1932	VSP\$SPT\$P\$Q\$AL\$SLKAV\$GPPQ\$TPRRH\$GLQAA\$PA\$E\$TLP\$THVTF\$SEK\$FVLD	1991
1367	-----	1366
1992	TG\$TIPASTPQGVKPV\$SS\$TPV\$VVT\$SV\$SAPPAP\$P\$P\$P\$P\$EPT\$KTVT\$QSL\$PAKEV	2051
1367	-----KTEAFQIOGR\$F\$SVVROC\$K\$S\$R\$ALAKIIP	1401
2052	VSSP\$SSPR\$P\$R\$E\$G\$TTL\$BQ\$P\$P\$Q\$PYTFL\$E\$K\$ARG\$F\$GVV\$RAC\$N\$ATGR\$F\$VAKI\$V\$P	2111
1402	YHPKDKTAVUREY\$EAL\$K\$LRH\$P\$LAQ\$LAAY\$LSPRH\$VLI\$LEL\$C\$G\$PELL\$P\$C\$LAER\$ASY\$S	1461
2112	YAA\$E\$K\$R\$V\$L\$Q\$E\$V\$L\$R\$TL\$H\$ER\$IM\$SL\$H\$EAYIT\$PY\$V\$L\$IA\$ES\$C\$N\$R\$EL\$C\$GL\$S\$DR\$F\$YS	2171
1462	E\$E\$K\$D\$YL\$W\$OM\$S\$AT\$V\$L\$N\$O\$HT\$L\$H\$LD\$R\$SE\$N\$M\$IT\$E\$Y\$N\$LL\$K\$V\$D\$D\$IGN\$A\$O\$S\$LO\$E\$K\$V\$L\$P\$S	1521
2172	EDD\$VAT\$Y\$V\$Q\$LG\$LYL\$G\$H\$V\$H\$UD\$IK\$PD\$N\$LL\$AP\$D\$N\$AL\$K\$IVD\$F\$G\$A\$F\$Y\$P\$Q\$AL\$R\$PL	2231
1522	DKF\$D\$Y\$ET\$M\$APEL\$B\$EQ\$G\$AV\$P\$D\$T\$W\$AI\$GV\$T\$AF\$IM\$S\$A\$Y\$F\$V\$S\$E\$G\$AR\$D\$Q\$LR\$K\$R\$GL\$V	1581
2232	GHR\$T\$G\$TLE\$F\$N\$APE\$V\$M\$V\$K\$E\$P\$IG\$S\$AT\$D\$W\$AG\$V\$LY\$IM\$LS\$GR\$S\$F\$F\$E\$P\$D\$Q\$E\$T\$E\$AR\$IV\$G\$GR\$F	2291
1582	EL\$R\$CY\$AGL\$SG\$VA\$F\$LR\$STL\$CAQ\$N\$G\$R\$C\$AS\$C\$L\$Q\$C\$P\$M\$TE\$E\$G\$P\$AC\$SR\$P\$AP\$T\$F\$P\$PARL	1641
2292	DA\$Q\$Y\$INT\$S\$AT\$L\$F\$UR\$K\$V\$L\$S\$V\$H\$P\$W\$R\$S\$F\$S\$LO\$Q\$LA\$H\$F\$W\$Q\$D\$AV\$IM\$K\$UR\$Q\$T\$T\$F\$T\$TNRL	2351
1642	RVFVRNREKRALLYKHNLL	1661
2352	KEFLGEQRRRAEAAETHKV	2371

Search completed: April 23, 2004, 15:17:29
Job time : 69 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:05:32 ; Search time 28 Seconds
(without alignments)
5719.960 Million cell updates/sec

Title: US-10-697-263-2
Perfect score: 8740
Sequence: 1 MGCCRLGCGCSVAHSVSG.....RNREKRALLYKRHLAQVR 1665

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	702.5	8.0	1398	2 T25568	hypothetical prote
2	550.5	6.3	1176	2 JN0583	myosin-light-chain
3	544.5	6.2	1147	2 A59307	myosin-light-chain
4	532	6.1	1906	1 S68235	myosin-light-chain
5	531	6.1	6658	2 T13311	projectin fruit
6	523.5	6.0	2783	2 T34416	hypothetical prote
7	498	5.7	6831	2 A88852	protein unc-22 (im
8	498	5.7	6839	2 S57242	twitchin (similar
9	498	5.7	7160	2 T27935	hypothetical prote
10	465.5	5.3	608	2 A35021	myosin-light-chain
11	463.5	5.3	451	2 S49128	twitchin-like prot
12	456	5.2	1423	1 I37275	death-associated p
13	454.5	5.2	1398	2 T13741	hypothetical prote
14	451	5.2	371	2 JC7733	death associated p
15	450	5.1	610	2 A28798	myosin-light-chain
16	449	5.1	1051	1 JN0051	serine/threonine-s
17	442.5	5.1	26926	1 I38344	titin, cardiac mus
18	441.5	5.1	374	1 S50193	Ca2+/calmodulin-de
19	438	5.0	1734	2 A54502	microtubule-asso
20	427.5	4.9	1435	2 T32930	hypothetical prote
21	427	4.9	370	1 S57347	Ca2+/calmodulin-de
22	423.5	4.8	1211	2 T27522	hypothetical prote
23	418	4.8	414	2 JN0323	Ca2+/calmodulin-de
24	407.5	4.7	606	2 D96532	probable CDPK-rela
25	406	4.6	602	2 S60052	calcium-dependent
26	404.5	4.6	469	1 S17656	Ca2+/calmodulin-de
27	401.5	4.6	601	2 T46084	CDPK-related prote
28	401	4.6	529	1 S71774	calcium-dependent
29	399.5	4.6	473	1 A53036	Ca2+/calmodulin-de

30 398.5 4.6 708 2 T23616
31 398.5 4.6 1237 2 T45070
32 398 4.6 1192 2 T18611
33 394.5 4.5 348 2 T37321
34 391.5 4.5 608 2 T18445
35 389.5 4.5 474 1 TVRTC4
36 389.5 4.5 502 2 I52637
37 387 4.4 533 2 C32571
38 387 4.4 740 2 I38556
39 386.5 4.4 560 2 S51600
40 385 4.4 752 1 A32571
41 384.5 4.4 774 2 I48609
42 384 4.4 735 2 A53300
43 383 4.4 481 2 JEO377
44 381.5 4.4 888 2 A53118
45 381.5 4.4 1246 2 G82287

ALIGNMENTS

RESULT 1

T25568

hypothetical protein C24G7.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T25568

R;Goela, D.; Wilson, R.

submitted to the EMBL Data Library, February 1997

A;Description: The sequence of C. elegans cosmid C24G7.

A;Reference number: Z20052

A;Accession: T25568

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1398 <GOS>

A;Cross-references: EMBL:U88310; PIDN:AAB42336.1; GSPDB:GN00019; CESP:C24G7.5

A;Experimental source: strain Bristol N2; clone C24G7

C;Genetics:

A;Gene: CESP:C24G7.5

A;Map position: 1

A;Introns: 13/2; 132/2; 220/3; 316/2; 491/3; 558/3; 734/3; 842/1; 1103/3; 1213/2;

Query Match		8.0%;	Score 702.5;	DB 2;	Length 1398;
Best Local Similarity		22.2%;	Pred. No. 1.4e-15;		
Matches 366;		Conservative 215;	Mismatches 582;	Indels 485; Gaps 70;	
QY	204	AQAYRR	-----DILAALSHPLVTGLDQPE	TRKTLILILELCSBELLDLYRK	253
DB	2	AEQYEQKQRTLYANSTIDGLSLAH	PGV-----EIAE---	PX	35
QY	254	GVVTRAEVKYIQQLVEGLHYLHSG	VHLDIKPSNIMLVHPAREDIKIC	DFGPAQNI	TP 313
DB	36	GVNRETQVRFVQRLALAKXHXH	DLRIAHLDLRPETILL---QDD	KLADFGQARR	LLR 92
QY	314	AEIQFSQYSPFVSPFIQIQPVSE	ASDIWAMGVISLSLTCSPPFAGE	SDRATLNLV	373
DB	93	GLITGEIKGSPFVSPFVSRVPL	TATDMSTGVLTIVLTGLSPFH	GDNDNETLANV	D 152
QY	374	EGRVSSSMAHLSEDAKDFIKAT	QAPQAPSAOCLSHPW----	LKSMAEAEH	F 429
DB	153	SCQFD--SSEL--GNFSYDAG	DFVKLLTIPVSRULTVDALDHP	WINDKLTETP-----	204
QY	430	INTKQLKFLAASRQSRSLMSY	KSLVMRS-----IPELLRGP	-----PDSFSLGVA	RHL 479
DB	205	LSADTLRBEFYCHKWLE----	RRVFVQQTPEQILEALGPATA	QAQNAFVPEGR	RRP 259
QY	480	CR-----	DTGSSSSSSSSDNE-----	LAPFARAK	504
DB	260	AIYDYLRIQPKXPPTVEYVQ	PKRHPPTIDFEGQLIDGADF	REBEGTGFEGH	QPP 319
QY	505	SLPPSS-----VTHS-----	PLHPRGELRPSASLPEEA	EAE	535
DB	320	QIPFPQRENAAHDSRREHQ	PQHQGQFORIPVDQYGRPL	VDPR-YLNDPSH	RPSLLD 378

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1503 QY KVDVIGNAQSLSQEKVLSPDKFKQVLET--MAPEL-LSGQGAVPQTDTWAIQVTAIFIMLS 1559
1235 DB LKVDVFGRAQKVS-GAVKQVD-----FDYKNASPEFHIPETPVTVQSDWMGMGVVTFCLLA 1288
1560 QY AEPYVSSEGCARDLQRLKRLKVLRSRCVAGL-----SGCAVAFLRSLTCAQGWGRPCASS 1614
1289 DB GFHPPTSE--YDRESEIKENVINV-KCDPNLIPVNASQECLSFATWALKKSPVRMRTDE 1345
1615 QY CLQCQWLTEEGPACSRPAPVPTPTARLR 1642
1346 DB ALSHKFLSDPSWVRRESIKYSASRLR 1373

RESULT 2
UN0583
myosin-light-chain kinase (EC 2.7.1.117) 155K protein - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C:Accession: UN0583; PN0490
R: Kobayashi, H.; Inoue, A.; Mikawa, T.; Kuwayama, H.; Hotta, Y.; Masaki, T.; Ebashi, S.
J Biochem. 112: 786-791, 1992
A:Title: Isolation of cDNA for bovine stomach 155kDa protein exhibiting myosin light chain
A:Reference number: UN0583; NCBI:93203148; PMID:1284247
A:Accession: UN0583
A:Molecule type: mRNA
A:Residues: 1-1176 <KOB>
A:Cross-references: GB:S57131; NID:G298638; PIDN:AAB25794.1; PID:G298639
A:Experimental source: stomach
A:Accession: PN0490
A:Molecule type: protein
A:Residues: 44-55; 721-728; 828-851; 1002-1019 <K02>
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; fibronectin type III
C:Keywords: ATP; calmodulin binding; phosphotransferase
F:370-430/Domain: immunoglobulin homology <IMM1>
F:723-980/Domain: protein kinase homology <KIN>
F:731-739/Region: protein kinase ATP-binding motif
F:1083-1144/Domain: immunoglobulin homology <IMM2>

Query Match 6.3%; Score 550.5; DB 2; Length 1176;
Best Local Similarity 25.3%; Pred. No. 7, 9e-11;
Matches 145; Conservative 91; Mismatches 191; Indels 147; Gaps 10;

QY 45 SSLPALPG-----PSSQVTVIEDVQAQTGCTAQFAIISGDPOP 83
DB 468 SSSLPVLTGESDATVKKPAPKPTPPKAMPQIQIPEDQKVRAGESVELFGKVGAGTQPI 527
QY 84 SVTVTKDSVLVDSTRLSQQQEGTYSVLVRHVASKDAGVYTCIAQN----- 130
DB 528 TCTWKKFRKQIQDSHIIKVENSENQSGSKLTIRAAQEHGCGCTLLVENKLGSRQAQVNLTV 587
QY 131 -----TGGQVL-----CK-- 138
DB 588 VDKPDPAGTPCASDIRSSSITLSWYSGSYDGGSAQVSVEIWDSDVTKWKLATCRST 647
QY 139 -----AELLVLG--GDNEP-----DSEKQ-- 155
DB 648 SFNVQDLDPREYKPRVRAINVYGTSEPSQSELTALGEKPEEPKDEVEVSDDDKEPE 707
QY 156 -----SHRKLKHSFVEVEKEIGRGVFGVKRVQHKGNKILCAAKETIPLRSRTAQAY 207
DB 708 VDYRTVTNTEQKVSDFYDIEERLGGKFGQVFRVLVEKTKGIWAGKFKFVSAKEKENI 767
QY 208 R-ERDILAAALSHPLTGLLDQFETKTLILILELCSSELDRLYRKGV-VTEAEVKVI 265
DB 768 ROEISIMCLHHKPKVQCVDAAFEKANIWLVEISVGGELFERIIDEFELTERSCIKYM 827
QY 266 QQLVTEGLHYLHSHGVHLHDIKPSNITMLVHPAREDIKICDQFQAQNTIAEILQFSQGSPE 325
DB 828 KOISEGVYIHKQGVTHVLDLPENIMCVNKTGTRIKLIDFGLARLENAGSLKVLFGTPE 887
QY 326 FVSPHIIQONPVSEASDIWAMGVISYLSLTCSPPAGESDRATLLNLVLEGRVSWSSPMAA 385
DB 888 FVAPRVINVEPIGATDMSIGVICYILVSGISPPMGNDNETLANVTSATWDFDDEADP 947

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386 HLESDAKRTKATLQAPQAPSAACLSHPFLKSPAEBAHFINTYKQLKELLARSRWQ 445
948 EISDDAKFISNLKDKMKNRLNCTQCLQHPWLMDTKRMKAKLSKDKRMKYMARRKWQ 1007
446 RLSMSYKSLVMSRIPEL-----LRGPPDSP 471
1008 KTGNAVRAIGRLSSMAMISGLSRKSSSTGSP 1041
RESULT 3
A59307
myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 20-Jun-2000 #sequence revision 20-Jun-2000 #text_change 20-Jun-2000
C/Accession: A59307; A41674; B41674; A40210
R/Gallagher, P.J.; Herring, B.P.; Griffin, S.A.; Stull, J.T.
J. Biol. Chem. 266, 23936-23944, 1991
A>Title: Molecular characterization of a mammalian smooth muscle myosin light chain kinase
A/Reference number: A41674; MUID:192084694; PMID:1748666
A/Accession: A59307
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1147 <GAL>
A/Cross-references: GB:M76233; NID:g165703; PIDN:AAA73093.1; PID:g165704
A/Experimental source: dev stage Adult; sex Female; tissue type smooth muscle
A/Note: this revision submission is not cited in GenBank entry RABSMMLCKR, release 115
A/Accession: A41674
A/Molecule type: DNA
A/Residues: 1-22, 'CTA', 26, 'SRS', <GA>
A/Cross-references: GB:M76369
A/Note: this translation is not annotated in GenBank entry RABSMMLCKD, release 115
A/Note: this sequence has been revised in reference A40210
R/Gallagher, P.J.; Herring, B.P.; Griffin, S.A.; Stull, J.T.
J. Biol. Chem. 267, 9450, 1992
A/Reference number: A40210; MUID:92250555; PMID:1577772
A/Contents: erratum
A/Accession: A40210
A/Molecule type: DNA
A/Residues: 23-30 <GA>
A/Note: this is a revision to the sequence B41674 from reference A41674
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; fibronectin type III
C/Keywords: ATP; phosphotransferase; smooth muscle
F:343-403/Domain: immunoglobulin homology <IMM1>
F:694-951/Domain: protein kinase homology <KIN>
F:702-710/Region: protein kinase ATP-binding motif
F:1055-1116/Domain: immunoglobulin homology <IMM2>
Query Match 6.2%; Score 544.5; DB 2; Length 1147;
Best Local Similarity 23.7%; Pred. No. 1.2e-10;
Matches 149; Conservative 97; Mismatches 206; Indels 177; Gaps 10;
48 PALGPPSPMQVIEDVQATGTAQFEALISGDPPSVTWYKDSVOLVDSTRLSQOEGT 107
463 PRATPPQIPQPPQDQKVRAGVERLFGKVGATQPTCTTMMKFRKQIDSEHKVNSEA 522
108 TVSLVLRHVASKDAGVYTCIAQNTGGQVLCXKALLVLG----- 145
523 GSKLTILAAAROEHCYGLLVENKLSGRQAQVNLTVVDKPPDPAGTFCASDIRSSSLTSL 582
146 -----G 146
583 WYGVSSVDGSAVSQVSVLEINSDVDKMTLTCSTSNVEDLLPDREYKFRVRAINVG 642
147 DNEP-----DSEKQ-----SHRKLHSFYVEKKEI 171
643 TSEPSOESELTIVGSKPEBPXDEVEVSDDDKEPEVDYRTVTVTNTEQKVSDFYDIEERL 702

172 GRGVTFVVRVQHGKNKILCAAKFIPLRSRTRQAQYRRD-----ILAALSHPLVTGL 224
703 GSGKFGQVRLVEKKTGKIMAGKFF-----KAYSACEKENIPAEIGIMNCLHPKLVOC 756
225 LQGFTRKTLIILILCLCSSEBLLDRLYRKGV-VTEAEVKVYIQQLVEGLHYLHSGVHLH 283
757 VDAFEKANIWMVLEIVSGGELFERIIDDFELTERECIKYMRQISEGVYIHKQIVHL 816
284 DIKPSNLMVHPAREDIKICDFGAQNTIPABLOFSQYSGSPFVSPILIQNPVSEASDI 343
817 DLKPNIMCVNKTGTRIKILIDFGLARRLENAGSLKVLFGTPEFVAPEVINYEPIYSATDM 876
344 WANGVISYLSLTSSPFFAGESDRATLNLVLRGVSWSPPMAHLSEDAKDFIKATLQAP 403
877 WSGIVICVILVSGLSPFFGNDNETLANVTSATWDFDEAFDEISDDAKDFISNLLKDM 936
404 QAPSAACLSHPFLKSPAEBAHFINTYKQLKELLARSRWQSLMSYKSLVMSRIPEL 463
937 KRLDCTCLOLQHPWLMDTKRMKAKLSKDKRMKYMARRKWQKTGNVRAIGRUSSWAMI 996
464 LRGPDPSPSLGVARHLCLRDTCGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 523
997 -----SGLSRKSSSTG-----PTSPLT----- 1014
524 RPSASLPSEAEASERSTEAPA---PPASP 549
1015 --ARLETEEDVDSQAFLEAVAEKPHVKP 1041
RESULT 4
S68235
myosin-light-chain kinase (EC 2.7.1.117), 210K, nonmuscle - chicken
N:Contains: myosin-light-chain kinase, 108K, smooth muscle; telokin
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S68235; A43099; B44389; A44389; S28227; S78216; A35093; A25810; S11652
R/Watterson, D.M.; Collinge, M.; Lukas, T.J.; Van Eldik, L.J.; Birukov, K.G.; Stepanova, F.E.S. Lett. 373, 217-220, 1995
A>Title: Multiple gene products are produced from a novel protein kinase transcription re
A/Reference number: S68235; MUID:96033976; PMID:7589469
A/Accession: S68235
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1906 <WAT>
A/Cross-references: EMBL:X52876; NID:g992992; PIDN:CAA37056.1; PID:g992993
R/Shoemaker, M.O.; Lau, W.; Shattuck, R.L.; Kwiatkowski, A.P.; Matrisian, P.E.; Guerra-S
J. Cell Biol. 111, 1107-1125, 1990
A>Title: Use of DNA sequence and mutant analyses and antisense oligodeoxynucleotides to e
activity.
A/Reference number: A37099; MUID:90361738; PMID:2202734
A/Accession: A37099
A/Molecule type: mRNA
A/Residues: 649-1906 <SHO>
A/Cross-references: EMBL:X52876
R/Collinge, M.; Matrisian, P.E.; Zimmer, W.E.; Shattuck, R.L.; Lukas, T.J.; Van Eldik, L.
Mol. Cell. Biol. 12, 2359-2371, 1992
A>Title: Structure and expression of a calcium-binding protein gene contained within a c
A/Reference number: A44389; MUID:92236611; PMID:1373815
A/Accession: B4389
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1695-1906 <COL>
A/Cross-references: GB:M88284; NID:g212237; PIDN:AA53767.1; PID:g212238
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1750-1906 <CO2>
A/Cross-references: GB:M88283; NID:g211371; PIDN:AAA48647.1; PID:g211372
R/Yoshikai, S.I.; Ikebe, M.
Arch. Biochem. Biophys. 299, 242-247, 1992
A>Title: Molecular cloning of the chicken gizzard telokin gene and cDNA.
A/Reference number: S28227; MUID:93073972; PMID:1444462
A/Accession: S28227

QY 1331 MGYSSPSEQVLLG--GPHSLASBE---ESQGRSAQPLPSTKT-----FAFQTK 1374
Db 1399 ISEPSQSESVVKGQKEEELKEBEAEALSDDEKETEYVYRTVTINTQKVSDVYNIER 1458
QY 1375 IQGRFVSVRQCKWAKSGRALAAKII--PYHPKOKTAVLRVEALKGLRHPHQAOLHAAYL 1433
Db 1459 LGSKFGGVFLVKKTKVWAGFFXKAYSAREKINRDELSINWCUHHPKLVOQVDAFE 1518
QY 1434 SPRLVLILELCSGPPELLP--CLABRASVSESEVDYLMQMLSATQYLYHNQHILHDLRSE 1492
Db 1519 EKANIMVLEWVSGELFERIIDFELTERECIKYMQQISEGVYIHKQGIHVLDLKPE 1578
QY 1493 NMITEY--NULLKVDIGNAQSLSQE---KVLPSDKFDVLETWAPPELLSGQAGVPTDI 1547
Db 1579 NIMCVNKTGTSIKUIDFGLARLESAGSLKVLFTP-----EFVAPEVINYEPIGYETDM 1633
QY 1548 WAIGVTAFIMLSABVPVSSECARDIQLRKLGLVRL--SRCVAGLSGCAVAFRLSTLCAQP 1606
Db 1634 WSGIVCIVLVSGLSPFGMDNDNETLANVTSATWDFDEAFDEISDDAKDFISNLLKKDM 1693
QY 1607 WGRPCASSCLOCPWITEE 1624
Db 1694 KSLNCTOCLQHPWLQKD 1711

RESULT 5
Ti3931
projectin - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: Ti3931
R:Dailey J.; Southgate, R.; Ayne-Southgate, A.
J. Mol. Biol. 279, 201-210, 1998
A:Title: Structure of the Drosophila projectin protein: isoforms and implication for pro
A:Reference number: Z17815; MUID:98300339; PMID:9636710
A:Accession: Ti3931
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6658 <DAL>
A:Cross-references: EMBL:AF047475; NID:G33337430; PID:G33337431; PIDN:AAC27550.1
C:Genetics:
A:Gene: projectin
A:Cross-references: FlyBase:FBgn0005666
A:Map position: 4
A:Note: intron positions not resolved (incomplete sequence)
C:Keywords: muscle

Query Match 6.1%; Score 531; DB 2; Length 6658;
Best Local Similarity 20.7%; Pred. No. 1.6e-09;
Matches 277; Conservative 153; Mismatches 403; Indels 508; Gaps 46;

QY 158 REKLHSFYEVEKEIGRGVGFVKRVQHKNGKILCAAKFIPL-RGRTRAQAYRERDILAAL 216
Db 5707 QQSVYDRIDILEETGTGAFGVVHRCRERSTGNIFAAKFIPIVSHSVKDLIRREIDIMNQL 5766
QY 217 SHPLVTGLLDQPETRKTILILELCSSEBLLDLRYKRG-VVTEAFVKYIQQOLVEGLHYL 275
Db 5767 HHOKLINLHDAFEDDDMILILEFLSGGELFERITAEVGVVTEAEVINMRQICEGIRHM 5826
QY 276 HSHGVHLIDIKSNILMVHPAREDIKICDQFAQNIITPAELQFSQYGSPEFVSPILQON 335
Db 5827 HQONIHLDIKPENIMCOTRSTNVKLDIFGLATKLDNEVVKITITGREFGAEIVNRE 5886
QY 336 PYSEASDIWAGVIVSYLSITCSSPPAGESDRATLLNVLEGRVSWSPMAHLSDAKDFI 395
Db 5887 PVGFTYDMWATGVLSVYLLSGLSPFAGDNDQTLKNVACDWDFALESFKYISBEAKDFI 5946
QY 396 KATLQAPQARSAAQCLSHPHFLKMPABEAHFINTQKPELLARSEWQSLMSYKSL 455
Db 5947 RXLLVRNKEKRWTAHECLLHPWLTGDHSVAKQGE--NRD--RYLAYREKLRRKYEDREFL 6003
QY 456 V-----MRSIPELLRGPPDPSPSLGVARHLCRDTGGSSSSSSSSSDNELAPPARAKSLPP 508

Db 6004 LPIGRLSEYSSLRKLL-----MEKYKIH-----AVDRQAA-- 6036
QY 509 SPVTHSPILLHPGRFLRPGASLPPEEAASE--RSTEAPAPASPPEGAGPPAAQGCV-- 561
Db 6037 -----PRFVIRPSQFCYEQSVKFCRCIAIATPTLTWNNHNLQSVKFMCR 6086
QY 562 -----PRHSVIRSLFTHQAGESPEHGALAPGSRHRPARRHLLKGGYIAGALPLAEPLME 617
Db 6087 YVGDDYYFIINRVKPHDRGE-----YITRA----- 5111
QY 618 HRVLEEAAREEQATLLAKAPSFETALRLPASGTHLAPGHSLSHLEHSPSTPPRSEACG 677
Db 6112 -----ENHYGSRREVFLNVQP-----LP-----KEQPRYRTES-- 6140
QY 678 EAQRLPSAPSGGAPTRDMGHGPGSKQLPSTGGHPTAQPERSPSPWQOPAFCHPKQG 737
Db 6141 -----TPVR-----RREPLPYTFW----- 6154
QY 738 SAPOEGCSHPAVAPCPGSPFGCKEAPLVSPSPFLGQOPAPAPAKASPLDSKMP 797
Db 6155 -----QE-----ESETAPSTFLLRPV-----MQA 6175
QY 798 GD-----ISLPGRPKPGPCSPGASQSSQSSVSLRVSSQVGTPEPGPSLDAEWQBA 852
Db 6176 RDTCKLLCLSGKVP-----NVR-----WYKDG 6199
QY 853 EDLSDSPTLQRPQSVTMKPSLGRGGYAGVGYTFAFGDAGGLGQGPWWARIAW 912
Db 6200 RELSKYEYANTHSDGVVTFM----- 6219
QY 913 AVSSEEEQEEARAESEQOEAEARABSPLOVSGARPVEVGRAPTRSSPPTWEDIG 972
Db 6220 -----IIDCKP-----SDSG 6229
QY 973 QVSLVQIRLDGDAEADTISLDISEVDPAYNLSD--LY--DIKYLPEFMIFRKVPKS 1028
Db 6230 NVS--CKATNCHGTDETCVIVVEGKVTPEQQLAHNPLYSGDKYI----- 6275
QY 1029 AOPEPPSPMAEBELAFPEFTWPGELGPHAGLITEESESDVALLA---BAAVGRKK 1085
Db 6276 EQPIKAPLPIVTSRQYTS-----SSVQNTSEPDGKVNVSNSNSGISNKKK 6323
QY 1086 WSPSPRSLSLPHFGRLHPLDEPAELGLRERKASVEHISRLKGRPEGLEKEGPPRKKPGL 1145
Db 6324 YASNS--LQAPG-----SFSRSRSAT 6342
QY 1146 ASPLSLGLKSWDRAPTFRLRELSDETIVLQSVTLACQVSAQAAQATWSKDGAPLESSSR 1205
Db 6343 KELILPDDSLMCKPEFTKPLHDLTIHDSGEQLILTCYVKGDPEPQISWSKNGKSLSSD- 6401
QY 1206 VLISATLKN-FOLLITLVVVASDGLGVYTCVSNALGTVTTTGVL-----RKAER 1253
Db 6402 -ILDLYKNGIATLTINEVFPDEGVIITCTATNSVGAVETKCKLTIQPLDKNINKKVA 6460
QY 1254 PSSSP-----CPDIGVVADGVLLVW-----KPVESYGPVTYI 1286
Db 6461 GDNAPKIVSHLSRFVRRDGDVNLACRIIQAQHF-----VWLHNKKEIKPSKDF----- 6511
QY 1287 VQSLGSGSWTTLASDIFPCCVLTSLKSRGTYT-----FTTACVSKAGMGPYS 1336
Db 6512 -QVTNEANIVRLQIASIFP-----EDGGTYTCEAFNDIGESFSTCTINVTVPDET 6562
QY 1337 -----PSEQVLLGGPSHLASEESO-----GRSAQPLST-KTFAFQTOIQGRFS 1381
Db 6563 QPSFVKPPTSVSVLEGEFTTFCCEIDSELLNLVWLKQKPIDETLPRYFTKDGHRYSFA 6622
QY 1382 V-----VRQWEKA-SGRA 1394
Db 6623 VAKCNMDDVQYQAKAVSGKA 6643

734416
hypothetical protein F12F3.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34416
R:Fulton, B.; Wohldmann, P.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of C. elegans cosmid F12F3.
A:Reference number: Z21521
A:Accession: T34416
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2783 <FUL>
A:Cross-references: EMBL:U80022; PIDN:AAC25886.1; GSPDB:GN00023; CESP:F12F3.2
A:Experimental source: strain Bristol N2; clone F12F3
C:Genetics:
A:Gene: CESP:F12F3.2
A:Map position: 5
A:Introns: 45/3; 90/3; 451/3; 509/1; 2313/3; 2341/3; 2378/3; 2414/2; 2453/3; 2474/2; 252

Query Match 6.0%; Score 523.5; DB 2; Length 2783;
Best Local Similarity 20.6%; Pred. No. 1.2e-09;
Matches 364; Conservative 223; Mismatches 643; Indels 539; Gaps 73;

QY 48 PALGPPSMQ-VTIEDVQ-----AQTGTAQFAIIEGDPQPSVTWYKDSVQLVDSTRL 100
Db 50 PAAPGPAVEDQNVDSVRLRWAAPTNDGGSPVRNVTVMCTEKGKTWTKAEVTKQAFITL 109
QY 101 SQOQEGTYSVLRHVASKDAGVYTCLAQNTGQ--VLCKAELLY----- 143
Db 110 FNLVPGESYFRVR-----ADNTFGQSEPSDESELVVKNVSVVVEPKKE 156
QY 144 -----LGCNPEDEK--QSHR--RKLHSPYEVKEEIGRGVGFVRVQHK 186
Db 157 VKYKEGSDYERVAKDSPESEYKTIIDHRLPND-QAKYIHEELGKAGYGVYRATKA 216
QY 187 NKILCAAKFIPLRSRTAQ-AVRERDILAAALSHPIVNTGILDOFETRKTLIILIELCSEE 245
Db 217 TGTWAAKQVQVPGVKENVVHEISMNQLHHEKLLNLEAFDGMENWMLIEFVSQGE 276
QY 246 LLRLRY-KGVTEAEVKYIQLVEGLHYLHSHGVHLHDIKPSNLMVHPAREDIKID 304
Db 277 LFKXILEDLSMBEEVRDYMHOILGVSHMKHQIVHLDLKPENILLKAKNSNELKIID 336
QY 305 FGPAQNTITPAELOFQSOYSPFVSPRIIOQNVPSEASDIWAMGVISLSLTCSSPPFAGES 364
Db 337 FGLARKLDPKSVKLLFGTFPERCAPEVNVYQPVGLSTDWTVGVISYLLSGLSPFLGDS 396
QY 365 DRATLNVLEGRVSNWSPMAHLSEDAKDFIKATLQAPAPQAPPSAAQCLSHPWFLKMPA 424
Db 397 DEDTLANVSASDWDQDPDPSDWDVSDLAQDFICRLMIKDKRMSVQDALARHPWITQWPK 456
QY 425 EEAHFINTKQLKFLARSRWQSLMSYKSIILVMRSIPELLRGPDPSPSLGVARHLCDTG 484
Db 457 LDKSGVPARQKRNFLSLKRWSDLLFGL-----AKG-----AIFRLTW-- 499
QY 485 GSSSSSSSSNNELAPARAKSLP-----PSPVTH-----SPLLHP 519
Db 500 GVFERIAFTDAAPSVK-KQLEDIVANVGDIATLSCDVGVPSPKQVQYKDKELTVP 558
QY 520 RGLRPSASLPEAEAEASERSTAPAPSPAGGPPAAQ-----GCVPREHVSIRSLFVHQ 574
Db 559 -----SMKYDSFVNEGLAELTVKNIVESDAGVYTCRAITNDLGSIMTHAKLSV---X 606
QY 575 AGSPHEGALAPQSRHPA--RRHLLKGYTAGALPGLRPLMEHVRVLEAEAREEQAT 632
Db 607 ADSEKK-----KKSSTSPAVIEKKDKRKTSKVVVTEIMDPPNFHLLQDDEAKIGEPK 661
QY 633 LLAKAFSFTALRLPA-----SGTHLAPGHSHSL-EHDS-----PSTPRPSSEAC 676
Db 662 ILVVT---NTTLPPTVDVYHNGEHSINDSNVLRKDKGRVELHILSVSDTSDGKWKAV 718
QY 677 G-----EAQRLPSASGGAPIDMGHPQSGKQLPSTGCHPQTAQ----- 715

Db 719 GKNAFCECESEAKLTWVIPDG-----QYAPSFQKQLSDVKCSSESLILKLEVN 765
QY 716 -PERSPSPWQOPAPFCHPKQ-----GS-----APOEGCSHPAPVAPCPGGS 757
Db 766 IQANPAPBINWFRNESEIEHSHQHLQFDGSGNYSLTIIDAYAEADSGEYKCAKNKIGK 825
QY 758 FPPGCKEAPLVPSPFFLQGPAPAPAKASPPIDSKMGPQ-DISLQRPKPXGCSPPGS 816
Db 826 AHTVCCVRIEELS-----KRSKKIDGSKAPFRMQLP-TPREV----- 864
QY 817 ASQASSSQVSSLRVSSQVGTGPPSLDAEGWTOEAEADLSDTLQRPQOVWTRKFSL 876
Db 865 -----QCADLTVCSVSGT-PHENIK---WTXDDKPIDMSNKQVHENGVCILH--II 911
QY 877 GORGAGVAGVGTFAFGDAGMLGQGPMMARAWVSQSEEEQEEAEAREASQSEQQE 936
Db 912 GAR-----DDOGRVYCEAENIHGVAQSFVVVEIK-----EAYDKHVR 950
QY 937 ARAESPLPO-----VSARPVPVGRAPTRSSPEPTPWE-----IQQVSLVQ 978
Db 951 PXFLEPLVNCSTCEGNEVLECCVTGKIFPI-----TWYKDGKLLIENRMLQ 999
QY 979 IRDLG-----DAAADTISLDISEVDPAYLNLSDLYDIKILPFFPMI 1021
Db 1000 YTRKGVSRNLNIMVNMNDGEBYTCEAVNSLGKDFHTCTVKVDMG-LSKTRLTPVR--- 1055
QY 1022 FRKVPKSAQP-----EPP---SPMAEBELAE-----PPEPTWMPGELGP 1058
Db 1056 SRSRSRSPSVVGGEIQRPVTFEFLADATVTEGNRELEVEVDGPTPTPIEW---Y 1110
QY 1059 HAGLITSESDVALLAEAVGRKWSSPSRL-FHFQGR--HLPLDEPAE----- 1108
Db 1111 HDG-----KLVAE-----SRLRTYFDGRVAFLLKIYEAHEHNGQVY 1147
QY 1109 -----LGLRER-----VKA--SVEHISRLKGRPEGLEKEGPPRKLGLASFLSLGKS 1155
Db 1148 CKVSNKLGAVETRAIVVEAPDAAEHVQM----- 1177
QY 1156 WRAETPLRELSDEFVVL---QSVTLACVSAQAPAAQATSKDGAPL-ESSSRVLISAT 1211
Db 1178 -----PTFVKKQD---VLUKTAGETATFTCSYAPAAQVWHLNGKALQQTNSYKTRLP 1231
QY 1212 LKNFQLLTILVVAEDLVYTCVSVALGTVTTTVGLR-----KABRP----- 1254
Db 1232 DNTATLVIENTDELCTYTAVANNOFGDVHTSAQLTISGSEAKTAASLPYFIIEKLP 1291
QY 1255 -----SSSPGPDIGEVYADGVLLVMKPVESYGPVTYVOCSEGGSGWTT 1298
Db 1292 KINVEGATLSIQADLNGSPIPEV-----VWLKDNSELVESDRIQMKCDGVNYQL 1341
QY 1299 LASDIFDCCLTSKLSRGTYTFTTACVSKAGMGPSPSPSQVLLGGPSHLASEESQ-- 1356
Db 1342 LVRDV-----GLEDEGTVTI-TAENKGI-----QNTESVTVTKSEYKKEKKKV 1388
QY 1357 -----GRSAOPLPS-----TKTFAFOTOIQRGFSVVRQC-----WEK-ASG 1392
Db 1389 EKKDGGKKKPGPGLPFRSGASKTEQVTMAPDASEGPADSYEVERCPCDQREWVSCGT 1448
QY 1393 RALAAKIIPYHP-----KQTAVLREYALKGLRHPHLAQLHAAYLSPRHVLIL 1442
Db 1449 KSLELEIKGLTPNTEYIFRVAGKNKGIGEMSEMTSTLKTASVQAPQFTISPOSKI--- 1505
QY 1443 ELCSGPELLPLCAERASYSSESEVDYLWMLSATQYLN-----QHILH 1486
Db 1506 -----IANDDEFEIATVFSGTPTSPVKWYKENIQLVPEKIDVATSTSSILN 1554
QY 1487 LDLRSENMIITEYNLLKVVLDLGNQASLSQ 1515
Db 1555 LKSOBEN---GTFNCLNIENELQASASQ 1580

A88852
 Protein unc-22 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: A88852
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites Genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: A88852
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-6831 <STO>
 A:Cross-references: GB:chr_IV; PIDN:CAA98081.1; PID:3861830; GSPDB:GN00022
 C:Genetics:
 A:Gene: unc-22
 A:Map position: 4
 C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;
 Query Match 5.7%; Score 498; DB 2; Length 6831;
 Best Local Similarity 20.4%; Pred. No. 1.8e-08;
 Matches 394; Conservative 256; Mismatches 708; Indels 572; Gaps 91;
 QY 51 PGPPSVQV-TIEDVQQTGTAQFE-AITGGPQPSVWYKDSVOLVDSR-LSQQQEGT 107
 DB 4508 PGPIFDNNKQITVRAGETIIRIPYAGGAPKPIIDLFNGSPIFENERTVVDVNRG- 4566
 QY 108 TYSLVLRHVASK-DAGVYTCLAQNTGGQVLCALVILGDNEDP-----SEKQSHRRK 160
 DB 4567 --BIVITTTGSKRSKSGYKISATNKYKDKTKLVNFVLDAPKPTGPIRATDIQADAMT 4624
 QY 161 LHSFYEVKEIRGVGFVGRVYKQHKNKILCAAKFI-----PLSRTRAQAY 207
 DB 4625 L-SWRPPKONGDAITNVYVETKPGDWTYVGHVGTTLVRVNDANTPYEFVRABNQ 4693
 QY 208 -----RERDILAALSHPLVT-----GLDQFFTRKTLILI----- 237
 DB 4684 YGVGEPLTDDAIVAKNPFDPGAPQPEAVETSEAITLQWTRPTSDGGAPIQYVIEK 4743
 QY 238 LELCSSF-----ELLRLRYKGVVT-----EAQVYVYIQLVGLVHLS----- 277
 DB 4744 REVGSFTWKAAGNLTIDTKHRTVGLTPKTYEFVRAAY-NAAGGEYSVMSVITADNA 4802
 QY 278 -----HGVHLHDI-----KPSNLMVHPAREDIKIDFGPAQN-ITPAE-----LQFSQ 320
 DB 4803 PTRPKINMGMLTRDILAYAGERAKILVPPAASPAPKV-TFSKGENKISFTDPFRVKEYS- 4860
 QY 321 YGSPFVSPPIIQNPFVSEASDIWAGVLSYLSLTCSPFAGESDRATLLNVLRGVSW 380
 DB 4861 ----DEFLATITIEK-----SELTD-----GGLYFVELENSQ-----GSDSASIRLKVVD-----XPA 4903
 QY 381 SPMAHLSADKDFIKATLQAPQAPRSPAAQCLSH-----PW-----FLKSMP 423
 DB 4904 SPOHIRVEDIAPDC--CTLYWPPSDGGSPITNYIVEKLDLRHSDGKWKVSSFVRNLN 4961
 QY 424 ABEAHFINTKQAFLLARSRWORSL--MSYKSIILVMR--SIPELLRGPP----- 468
 DB 4962 YTVGGLIKONRYFRV-RAETQVGVSEPCELADVVAKYQVEVFNQPEAPTVRKDSTWA 5020
 QY 469 -----DPSLGVARHL-----CRDTGSSSSSSSSSNNELAPFAKSLPPSVTHSPIL-- 517
 DB 5021 ELEWDPDRDGGSKIIIGYQVYRDTSSGRWINAKMDLSEQCHARVTGLRQNGEFEFFRIIAK 5080
 QY 518 HPRGFLRPSASLPEEABASERSTEAPAPASPEGAGPP--AAQGCVRHRSVIRSLFVHQ 574
 DB 5081 NAAGFSKPS--PPSERCQIKRFGP-----PGPIHVGAKSIGRNHCTIT- 5123
 QY 575 AGSPSEHGALAPGSRHRHARRHLKGGYIAGALPGLREPLMEH-----RYLEBEAAREE 629
 DB 5124 -----WMAF-----LEDGG--SKITGVNVEIREYVGTSLWTVASDYNVREP 5161

QY 630 QATL--LAKAPSE-TAURLPASGTHLAPGHSHLSLEHDSPTPTSPSSACGEAQLRPSAP 686
 DB 5162 EFTVDKLRFNDFYFRVVAINAAG-----KGIPSLP 5192
 QY 687 SGGAPIRDGHGPGQKQLPSTGCHP-GTAQP-----ERSPDSPW---GQAP 730
 DB 5193 SGPIKIQESS--GSR--POIVVKEDTAQPNRBAVTCBAVGPETARMLNRLP 5247
 QY 731 FCHPKGSAFQSGCSPHAPVPCPGSPGSCCK-----EAPLVSPSPFLQOP 778
 DB 5248 EBSRYFEASD-----GVYKFTKEVMDIDAGEYTVSVSNPY-GSD 5287
 QY 779 QAPPAPAKASPLDSKMGFGDISLPRPKPGPCSPGSGASQASQSSQVSLRVSGSQVTE 838
 DB 5288 TATANLVQAPVIEKDVNTI-LP-----SGDIVRLAIYES--GTA 5326
 QY 839 PGPSLDAEGTQAEADLSDSIPTLQRPQEQ-----VTMRKFSLGRGGY-----AGVAGYT 890
 DB 5327 P-----FRHSLVLRSEIDMDHRTIIVFDDHILITIPALSVREAGRYEYTVSNDGSEAT 5382
 QY 891 FAFGGDAGM-----LQGGPMWARIANA-----VSQSE--- 918
 DB 5383 TGFMLNVTGLPEAPOPLHISNIGPSTATLSWRPPTDGGSKITSYVVEKRLSKDEWVT 5442
 QY 919 -----ESEQEBAEASQSESQEABARASPLPOYSARVPVGVGAPTRSS 962
 DB 5443 VTSNVKDMNYIVTGLFENHEYEFVSAQNGIGA-----PLVSEHPI--IARLPDPP 5494
 QY 963 PEPTWEDI-----GVSLVQIARDLSG-----DAEAAATISLDSIYEDPAYLN 1005
 DB 5495 TSPLNLEIVQVGDDVYTLWSORPLSDGGRLRGYIVEQEEDHEWFCRNQNPSPNNYN 5554
 QY 1006 LSDLVD--IKLPPF-----EFMLPRKPKSAQPEPPSMA----- 1038
 DB 5555 VFNLDGGRKYRVRVANDAGLSLAELODTLFOASGGEGFKIVPLUSDLINEVGRCVT 5614
 QY 1039 -EEELAEPEPTWPW--PGEL-----OPHAGLEITE-ESEDDVALLABAAYVR 1082
 DB 5615 FECEISGSPRPEYRKFCKELVDTSKYTLINKDKQVLIINDLTSDADYTCRATN-- 5672
 QY 1083 KKKWSPSRSLPHFGRHLPLDEPAELGLRERVASVEHISRLKGRPEGLEKGGPREKK 1142
 DB 5673 ----SSGTRS-----TRANLEIKTKPRVFI-----PKYH 5698
 QY 1143 PGLASFRISGLKSWDRAPTFRLSDETIVLGQSVACQVSAQAPAAQATWSDGABLES 1202
 DB 5699 GGYEAQK-----GETIELKIPYKAYFQGEARWTKDGEKIEN 5734
 QY 1203 SSRVLISATLKNFQLLTILVVVAEDLVYTCVSNALGTVTITGVLRKAERPPSSPCPD 1262
 DB 5735 NKSFSIT-TDDKFAELRLSNASREDYGEYRVVENSVDSDSGTVNVTADVPEPRFPII 5793
 QY 1263 GEYVAGVLLVWKPVEYSGPVYIVQCSLE-----GGSWTTLASDIFDCCVLTSLK-LSRG 1316
 DB 5794 ENILDEAVILSWKPPALDGG-SLVNTYTIKREAMGGSWSPCAKSRY--TYTTTIEGLRAG 5850
 QY 1317 GTYTERTACVSKAGMPYSSPSEOVLLGGPS--HLASEBESQGRSAQ----- 1361
 DB 5851 KYEYRIIAENKHGSKCEPTAPVLIPGDERKRRGYDVBQGIYRGRKTVSSNYDNY 5910
 QY 1362 -----PLP-----STKTFATQIQGRFSPVVRQCKEASGRALAAK-IIPYPH 1404
 DB 5911 VFDIMKQYPOQVEIKHDHLDHDIHEELGTGAFGVYHVRTERATGNFAAKVMTTPE 5970
 QY 1405 KDKTAVLREYEAALKRHPHQAALHAAYLSPRHLVILELCSGPPELLPCLA-ERASYSSES 1463
 DB 5971 SDKETVRKEIQTMSVLRHPTLVNLDHAFEDDNNMVMIVFMSGGELFEKVADENKMSD 6030
 QY 1464 EYKDYLMQWLSATQVYLNQHLHLDLSENMIIT--EYNLLKVVLDLNAQSLSOEKVLPS 1521
 DB 6031 EAVEYMRQVCKGLCHMHENNYVHLDPENIMFTKESNELKLDIFGLTAFLD-----PK 6085
 QY 1522 DRFK--DYLETMAPELLEGGQGAVPQTDIWAIGVTAFTMLSAEYFVPSSEGAQDIQRLRK 1578

C-Comment: Lack of unc-22 leads to a constant twitching of the body muscles.

C-Genetics:
A:Gene: unc-22; CESP:ZK617.1a
A:Map position: 4
A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 612/3; 669/1/3; 6776/1; 6808/3

C-Superfamily: twichin; fibronectin type III repeat homology; immunoglobulin homology;
C-Key words: ATP; autophosphorylation; duplication; muscle; phosphotransferase; serine/threonine kinase; myosin-like domain; protein kinase A; protein kinase B; protein kinase C; protein kinase D; protein kinase E; protein kinase F; protein kinase G; protein kinase H; protein kinase I; protein kinase J; protein kinase K; protein kinase L; protein kinase M; protein kinase N; protein kinase O; protein kinase P; protein kinase Q; protein kinase R; protein kinase S; protein kinase T; protein kinase U; protein kinase V; protein kinase W; protein kinase X; protein kinase Y; protein kinase Z; protein kinase AA; protein kinase AB; protein kinase AC; protein kinase AD; protein kinase AE; protein kinase AF; protein kinase AG; protein kinase AH; protein kinase AI; protein kinase AJ; protein kinase AK; protein kinase AL; protein kinase AM; protein kinase AN; protein kinase AO; protein kinase AP; protein kinase AQ; protein kinase AR; protein kinase AS; protein kinase AT; protein kinase AU; protein kinase AV; protein kinase AW; protein kinase AX; protein kinase AY; protein kinase AZ; protein kinase BA; protein kinase BB; protein kinase BC; protein kinase BD; protein kinase BE; protein kinase BF; protein kinase BG; protein kinase BH; protein kinase BI; protein kinase BJ; protein kinase BK; protein kinase BL; protein kinase BM; protein kinase BN; protein kinase BO; protein kinase BP; protein kinase BQ; protein kinase BR; protein kinase BS; protein kinase BT; protein kinase BU; protein kinase BV; protein kinase BW; protein kinase BX; protein kinase BY; protein kinase BZ; protein kinase CA; protein kinase CB; protein kinase CC; protein kinase CD; protein kinase CE; protein kinase CF; protein kinase CG; protein kinase CH; protein kinase CI; protein kinase CJ; protein kinase CK; protein kinase CL; protein kinase CM; protein kinase CN; protein kinase CO; protein kinase CP; protein kinase CQ; protein kinase CR; protein kinase CS; protein kinase CT; protein kinase CU; protein kinase CV; protein kinase CW; protein kinase CX; protein kinase CY; protein kinase CZ; protein kinase DA; protein kinase DB; protein kinase DC; protein kinase DE; protein kinase DF; protein kinase DG; protein kinase DH; protein kinase DI; protein kinase DJ; protein kinase DK; protein kinase DL; protein kinase DM; protein kinase DN; protein kinase DO; protein kinase DP; protein kinase DQ; protein kinase DR; protein kinase DS; protein kinase DT; protein kinase DU; protein kinase DV; protein kinase DW; protein kinase DX; protein kinase DY; protein kinase EZ; protein kinase FA; protein kinase FB; protein kinase FC; protein kinase FD; protein kinase FE; protein kinase FF; protein kinase FG; protein kinase FH; protein kinase FI; protein kinase FJ; protein kinase FK; protein kinase FL; protein kinase FM; protein kinase FN; protein kinase FO; protein kinase FP; protein kinase FQ; protein kinase FR; protein kinase FS; protein kinase FT; protein kinase FU; protein kinase FV; protein kinase FW; protein kinase FX; protein kinase FY; protein kinase FZ; protein kinase GA; protein kinase GB; protein kinase GC; protein kinase GD; protein kinase GE; protein kinase GF; protein kinase GG; protein kinase GH; protein kinase GI; protein kinase GJ; protein kinase GK; protein kinase GL; protein kinase GM; protein kinase GN; protein kinase GO; protein kinase GP; protein kinase GQ; protein kinase GR; protein kinase GS; protein kinase GT; protein kinase GU; protein kinase GV; protein kinase GW; protein kinase GX; protein kinase GY; protein kinase GZ; protein kinase HA; protein kinase HB; protein kinase HC; protein kinase HD; protein kinase HE; protein kinase HF; protein kinase HG; protein kinase HH; protein kinase HI; protein kinase HJ; protein kinase HK; protein kinase HL; protein kinase HM; protein kinase HN; protein kinase HO; protein kinase HP; protein kinase HQ; protein kinase HR; protein kinase HS; protein kinase HT; protein kinase HU; protein kinase HV; protein kinase HW; protein kinase HX; protein kinase HY; protein kinase HZ; protein kinase IA; protein kinase IB; protein kinase IC; protein kinase ID; protein kinase IE; protein kinase IF; protein kinase IG; protein kinase IH; protein kinase II; protein kinase IJ; protein kinase IK; protein kinase IL; protein kinase IM; protein kinase IN; protein kinase IO; protein kinase IP; protein kinase IQ; protein kinase IR; protein kinase IS; protein kinase IT; protein kinase IU; protein kinase IV; protein kinase IW; protein kinase IX; protein kinase IY; protein kinase IZ; protein kinase JA; protein kinase JB; protein kinase JC; protein kinase JD; protein kinase JE; protein kinase JF; protein kinase JG; protein kinase JH; protein kinase JJ; protein kinase JK; protein kinase JL; protein kinase JM; protein kinase JN; protein kinase JO; protein kinase JP; protein kinase JQ; protein kinase JR; protein kinase JS; protein kinase JT; protein kinase JU; protein kinase JV; protein kinase JW; protein kinase JX; protein kinase JY; protein kinase JZ; protein kinase KA; protein kinase KB; protein kinase KC; protein kinase KD; protein kinase KE; protein kinase KF; protein kinase KG; protein kinase KH; protein kinase KI; protein kinase KJ; protein kinase KK; protein kinase KL; protein kinase KM; protein kinase KN; protein kinase KO; protein kinase KP; protein kinase KQ; protein kinase KR; protein kinase KS; protein kinase KT; protein kinase KU; protein kinase KV; protein kinase KW; protein kinase KX; protein kinase KY; protein kinase KZ; protein kinase LA; protein kinase LB; protein kinase LC; protein kinase LD; protein kinase LE; protein kinase LF; protein kinase LG; protein kinase LH; protein kinase LI; protein kinase LJ; protein kinase LK; protein kinase LM; protein kinase LN; protein kinase LO; protein kinase LP; protein kinase LQ; protein kinase LR; protein kinase LS; protein kinase LT; protein kinase LU; protein kinase LV; protein kinase LW; protein kinase LX; protein kinase LY; protein kinase LZ; protein kinase MA; protein kinase MB; protein kinase MC; protein kinase MD; 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protein kinase OH; protein kinaseOI; protein kinase OK; protein kinase OL; protein kinase OM; protein kinase ON; protein kinase OP; protein kinase OQ; protein kinase OR; protein kinase OS; protein kinase OT; protein kinase OU; protein kinase OV; protein kinase OW; protein kinase OX; protein kinase OY; protein kinase OZ; protein kinase PA; protein kinase PB; protein kinase PC; protein kinase PD; protein kinase PE; protein kinase PF; protein kinase PG; protein kinase PH; protein kinase PI; protein kinase PJ; protein kinase PK; protein kinase PL; protein kinase PM; protein kinase PN; protein kinase PO; protein kinase PP; protein kinase PQ; protein kinase PR; protein kinase PS; protein kinase PT; protein kinase PU; protein kinase PV; protein kinase PW; protein kinase PX; protein kinase PY; protein kinase PZ; protein kinase QA; protein kinase QB; protein kinase QC; protein kinase QD; protein kinase QE; protein kinase QF; protein kinase QG; protein kinase QH; protein kinase QI; protein kinase QJ; protein kinase QK; protein kinase QL; protein kinase QM; protein kinase QN; protein kinase QO; protein kinaseQP; protein kinase QS; protein kinase QT; protein kinase QU; protein kinase QV; protein kinase QW; protein kinase QX; protein kinase QY; protein kinase QZ; protein kinase RA; protein kinase RB; protein kinase RC; protein kinase RD; protein kinase RE; protein kinase RF; protein kinase RG; protein kinase RH; protein kinase RI; protein kinase RJ; protein kinase RK; protein kinase RL; protein kinase RM; protein kinase RN; protein kinase RO; protein kinase RP; protein kinase RQ; protein kinase RR; protein kinase RS; protein kinase RT; protein kinase RU; protein kinase RV; protein kinase RW; protein kinase RX; protein kinase RY; protein kinase RZ; protein kinase SA; protein kinase SB; protein kinase SC; protein kinase SD; protein kinase SE; protein kinase SF; protein kinase SG; protein kinase SH; protein kinase SI; protein kinase SJ; protein kinase SK; protein kinase SL; protein kinase SM; protein kinase SN; protein kinase SO; protein kinase SP; protein kinase SQ; protein kinase SR; protein kinase SS; protein kinase ST; protein kinase SU; protein kinase SV; protein kinase SW; protein kinase SX; protein kinase SY; protein kinase SZ; protein kinase TA; protein kinase TB; protein kinase TC; protein kinase TD; protein kinase TE; protein kinase TF; protein kinase TG; protein kinase TH; protein kinase TI; protein kinase TJ; protein kinase TK; protein kinase TL; protein kinase TM; protein kinase TN; protein kinase TO; protein kinase TP; protein kinase TQ; protein kinase TR; protein kinase TS; protein kinase TT; protein kinase TV; protein kinase TV; protein kinase TW; protein kinase TX; protein kinase TY; protein kinase TZ; protein kinase UA; protein kinase UB; protein kinase UC; protein kinase UD; protein kinase UE; protein kinase UF; protein kinase UG; protein kinaseUH; protein kinase UK; protein kinase UL; protein kinase UM; protein kinase UN; protein kinase UO; protein kinase UP; protein kinase UQ; protein kinase UR; protein kinase US; protein kinase UT; protein kinase UU; protein kinase UV; protein kinase UW; protein kinase UX; protein kinase UY; protein kinaseUZ; protein kinase VA; protein kinase VB; protein kinase VC; protein kinase VD; protein kinase VE; protein kinase VF; protein kinase VG; protein kinase VH; protein kinase VI; protein kinase VJ; protein kinase VK; protein kinase VL; protein kinase VM; protein kinase VN; protein kinase VO; protein kinase VP; protein kinase VQ; protein kinase VR; protein kinase VS; protein kinase VT; protein kinase VU; protein kinase VW; protein kinase VX; protein kinase VY; protein kinase VZ; protein kinase WA; protein kinase WB; protein kinase WC; protein kinase WD; protein kinase WE; protein kinase WF; protein kinase WG; protein kinase WH; protein kinase WI; protein kinase WJ; protein kinase WK; protein kinase WL; protein kinase WM; protein kinase WN; protein kinase WO; protein kinase WP; protein kinase WQ; protein kinase WR; protein kinase WS; protein kinase WT; protein kinase WX; protein kinase WY; protein kinase WZ; protein kinaseXA; protein kinase XB; protein kinase XC; protein kinase XD; protein kinaseXE; protein kinase XF; protein kinase XG; protein kinaseXH; protein kinase XK; protein kinase XL; protein kinase XM; protein kinase XN; protein kinase XO; protein kinase XP; protein kinase XQ; protein kinase XR; protein kinase XS; protein kinase XT; protein kinase XU; protein kinase XV; protein kinase XW; protein kinase XY; protein kinase XZ; protein kinaseYA; protein kinase YB; protein kinase YC; protein kinase YD; protein kinase YE; protein kinase YF; protein kinase YG; protein kinase YH; protein kinase YI; protein kinase YJ; protein kinase YK; protein kinase YL; protein kinase YM; protein kinase YN; protein kinase YO; protein kinase YP; protein kinase YQ; protein kinase YR; protein kinaseYS; protein kinase YT; protein kinase YU; protein kinase YV; protein kinase YW; protein kinase YX; protein kinase YY; protein kinase YZ; protein kinaseZA; protein kinase ZB; protein kinase ZC; protein kinase ZD; protein kinase ZE; protein kinase ZF; protein kinase ZG; protein kinaseZH; protein kinase ZK; protein kinase ZL; protein kinase ZM; protein kinase ZN; protein kinase ZO; protein kinase ZP; protein kinase ZQ; protein kinase ZR; protein kinase ZS; protein kinase ZT; protein kinase ZU; protein kinase ZV; protein kinase ZW; protein kinase ZX; protein kinase ZY; protein kinase ZZ

Query Match 5.7%; Score 498; DB 2; Length 6839;
Best Local Similarity 20.4%; Pred. No. 1.8e-08;
Matches 394; Conservative 256; Mismatches 708; Indels 572; Gaps 91;

QY 51 PGPSPMQV-TIEDVAQTGGTAQFE-AIIEDGPPSVTWYKDSVOLVDSTR-LSQQQEQT 107
DB 4516 PGRPIFDINLKDIITVRAGETIQIRIPYAGNPKRPIDLFNGNSPIFENERTVVDVNP- 4574
QY 108 TSYLVLRHVASK--DAGVYTCLAQTGGVLCCKAEALLVLGGDNPD-----SEKSHRRK 160
DB 4575 --EIVITTGTGSRSDAGEKYISATNKYGOKTCUKLVFVLDAPGKTGTFIRATDQADAMT 4632
QY 161 LHSFYEVKEETGRGVFGFVKRVQRKGNKILCAAKFI-----PLRSRTAQAY 207
DB 4633 L-SWRPPXDNGDAITNYVWEKRTPGGDWTVGHPVTTLVRNLDMANTPYEFVRVAENQ 4691
QY 208 -----REEDIILAALSHPLVT---GLLDDQETKTKILLI----- 237
DB 4692 YGVGEPLTDPAIVANKNFDTTPGAPQDEAVETSEEALTQWTRPTSDGGAPIOGYVIEK 4751
QY 238 LELCSSE-----ELLRLRYKGVVT-----EAFFKVYIQQLVEGHYLHS----- 277
DB 4752 REVSGTEMTKAAGFNILDTHRVVLTGTPKTYEYERVAAY-NAAGQGEYSVNASVPITADNA 4810
QY 278 -----HGVLHLDI-----KPSNILMVHPAREDIKICDFGAQN-IIPAS-----LOFSQ 320
DB 4811 PTRPKINMGMLTRDILAYAGERAKILVPFASPAPKV-TFSKGKNKSPTDPVKVEYS- 4868
QY 321 YGSPFPVSPEIQONPVSEASDIWAMGVISYLSITCSPPFAGESDRATLLNVLSGRVWS 380
DB 4869 ---DFLATLATEK---SELTD---GGLYFEVELNSQ---GSDSASIRLKWVD---KPA 4911
QY 381 SPMAHLSEDADKFIAKLQAPARPAPSAQCULSH-----PW-----FLKSMP 423
DB 4912 SPQHIRVEDIADF-CCTLYMPPSSDGGSPTINYIVEKLDRHSDGWKXVSFVRNLN 4969
QY 424 ABEAHFINTKQLKELLARSQRSL---MSYKSIILVMR---SIPELLRGPP----- 468
DB 4970 YTVGGLIKDNRYFRFV-RAETQYGVSEPCELADVVAKYQFEVNPQPEAPTVRDKDSTWA 5028
QY 469 ----DSPSLGVARHL-----CRDTGGSSSSSSSDNELAPFAKSLPPSPVTHSPLL-- 517
DB 5029 ELENDPPRDGSKILGYOVQYEDTSSGRWINAKMDLSQCHARTGLRQNGEEFRIIAK 5088
QY 518 HPRGFRLPSASLPBEAESERSTAPAPSPGEGAGP---AAOGCVPRHSVIRSFLFHQ 574
DB 5089 NAAQFSPKPS---PPSERQLKSRFGP-----PGPPIHVGAKSIGRNHTCIT----- 5131
QY 575 AGESEPHEGALAFGRHRPARRHLLKGGYTAGALPGLREPLMEH-----RVLEBEAAREE 629
DB 5132 -----WMAP-----LEDGG---SKITGYNVEIREYGSTLWTVASDVNVREP 5169
QY 630 QATL--LAKASFPE-TALRLPASGTHLAPHGSHSLEHDSPTPRPSSEACGEAOBLPSAP 686
DB 5170 E

Db 5201 SGPIKIQESG---GSR--PQIVVKPETAQPNYRAVFTCEAVCRPEPTARWLNRGRLP 5255
Qy 731 FCHPKQSAPOEGCSGPHPAVACPSPGPFPGCSCK-----EAPLVSPSPFLGP 778
Db 5256 ESSRYRFEASD-----GVYKFTIKVEMDIDAGEYTVVEVSNPY-GSD 5295
Qy 779 QAPAPAKASPPLDSKMGCGDISLPGRPKPCGSPGCSASQASSOVSSLRVSSQVGTG 838
Db 5296 TATANLVVQAPPVIEKDVNTI-LP-----SGDLVRLKIYFS--GTA 5334
Qy 839 PGPSLDAEGMTQEAEDLSDSPTLQRPQEQ---VTMKFSLGGRGY----AGVAGYGT 890
Db 5335 P-----FRHSLVLRNEEDMDHPTIRIVFDDHILITIPALSVREAGRYEYTVSNDSEAT 5390
Qy 891 PARCGDAGGM-----LGQCPMKARIATA-----VSQSB--- 918
Db 5391 TGFNLVNTGLPEAPCGPLHISNIGPSTATUSWRPPTVDGSGKITSYVVERKDLKDEWVT 5450
Qy 919 -----EEQCEARAEASQSEQCEARAESELPQVSARPPVEVGRAPTRSS 962
Db 5451 VTSNVKQMYIVTGLFENHNEYFRVSAQENIGCA-----PLVSEHPI--IARLPDPDP 5502
Qy 963 PEPTPWEDI---GVSLVQIQRDLSG-----DAAADTISLDISEVDPAVLN 1005
Db 5503 TSPNLNLEIVQVGGDYVTLVSWORPLSDGGRGRLRGYIVKQEBEHEWFRCNQSPPNYN 5562
Qy 1006 LSDLYD---IKYLP-----EFMIFRKVPKSAQPEPSPMA----- 1038
Db 5563 VPNLIDGRKYRYFVANDAGLSDLAELDQTLFQASGSGEGPKIVSPLSDLNEBVGRCVT 5622
Qy 1039 -EEELAEPEPTWPH---PGEL-----GFHAGLEITE-ESDVDALLAEAAVGR 1082
Db 5623 FCEETSGSPREYRWFKGCKELVDTSKYTLINKGDKQVLIINDLTSDDADSYTCRATN-- 5680
Qy 1083 KRKWSPPSRLFFHPPGRHLPLDEPAELGLRRVRKASVEHISRLKPRGLEKEGPPRKK 1142
Db 5681 ----SSGTRS-----TRANLRIKPRVFI-----PKYH 5706
Qy 1143 PGLASFRSLGKSWDRAPTFLRELSDETIVLQGSVTLACQVSAQAPAAQWSKGAPLES 1202
Db 5707 GGYEAQK-----GETIELKIPYKAYPOGEARWTKDGEKIE 5742
Qy 1203 SRVLISATLKNFOLLITLVVAEDLGVYTCVSNALGTVTITGLRKAERPSPPCPDI 1262
Db 5743 NSKFSIT-TDDKFAFLRISNAREDYGEYRVVVENSGDSGTVNVTVADVPEPRPFI 5801
Qy 1263 GEVYADGVLLVMKPVESGPTVIYVQCSLE-----GGSWTTLASDIFDCCYLTSK-LSRG 1316
Db 5802 ENILDEAVILSNKPPALDGG-SLVNTVYTIKKEAAMGGSWSPCAKRY--TYTTIEGLRAG 5858
Qy 1317 GYTTTRTACVSKAGMPYSSPSQVLLGSPS---HLASEESQGRSAQ----- 1361
Db 5859 KQYEFRIIAENKHGQSKCEPTAPVLIIPGDERKRRGYDVEQGIKVRGKGTVSSNDYNY 5918
Qy 1362 -----PLP-----STKTFAPQIQGRFESVVRQWKEASGRALAAK-IIPYHP 1404
Db 5919 VFDIMKQYYPQVPEIKHDDVLDHYDIHEELGTGAFGVVHRVTERATGNFNAKFWMTPE 5978
Qy 1405 KDKTAVLRYEALKGLRPHLAQLAAVLSPRHVLILELCSGPPELLPCLA-ERASVSES 1463
Db 5979 SDKETVRKEIQTMSVLRHPTLVNLDAFEDDNNMVIYEFMSGGSELFKAVADENKMSD 6038
Qy 1464 EVKDYLMQMSLQVYLHNOHILHLDLRSNMIIIT-EVNLKAVVDLGNQAQSLSQEKLVP 1521
Db 6039 EAVEHWRQVCKGLCHGNNYVHLDLKPENIMFTYRSNELKLIIDFGLTAHLD-----PK 6093
Qy 1522 DKFK----DYLETWAPELLSSQGAVPQTDIWAJGVTAFLMLSAEYVPSSEGAARDLQGRUK 1578
Db 6094 QSVKVTGTGTAEPAAPEAVBAGKPGVYTDWMSVGLSYILLSGLSPFGGENDDETUNYKS 6153
Qy 1579 GLVRLSRC-----YAGLSGGAFLRSTLCAQPGWRGPCASSCLQCPWLTEEGPACSR 1630

Db 6154 -----CDWNMDSDAFSGISGDKDFIRKULLADPNTRMTIHOALEHPWLT-PGNAPGR 6205
Qy 1631 PAPVTFPTAR 1640
Db 6206 DSQI--PSSR 6213
RESULT 9
T27935
hypothetical protein ZK617.1b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T27935; T28031
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27935
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7160 <W12>
A:Cross-references: EMBL:Z73997; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b
A:Experimental source: clone ZK617
R:Harris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28031
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7160 <W12>
A:Cross-references: EMBL:Z73999; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
A:Experimental source: clone ZK829
C:Genetics:
A:Gene: CESP:ZK617.1b
A:Map position: 4
A:Insertions: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 591/3
3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3
C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology; I
Query Match 5.7%; Score 498; DB 2; Length 7160;
Best Local Similarity 20.4%; Pred. No. 1.9e-08;
Matches 394; Conservative 256; Mismatches 708; Indels 572; Gaps 91;
Qy 51 PGPPSQV-TIEDVQATGCTAQFE-AIEGDPQPSVTWYKDSVLVDSTR-LSQQOEGT 107
Db 4837 PGRPIFDINLKDITVRAGETIQRIPYAGNPKPIIDLFGNSPIFENERTVVDVNP- 4895
Qy 108 TYSVLVLRHASK--DAGVVTCLAQNTGGVLCVCAELLVGGDNEPD-----SEKQSHRRK 160
Db 4896 --EIVITTTGSKSDAGPKISATNKYKDTCKLVFVLDAPCKTGPTRATDIQADMT 4953
Qy 161 LHSFYEVKBEIGRGVFGVKRVQHKNGKILCAAKFI-----PLRSTRAQAY 207
Db 4954 L-SWRPPKONGGDAITNYVVEKRTPGCDWTVGHVPVGTTLVRNLDANTPYEFVRAENQ 5012
Qy 208 -----RERDILAAALSHPLVT-----GLDQFETRKTLILI----- 237
Db 5013 YGVGEPLTDDAIVAKNPPDTPGAPQPEAVETSEAILOWTRPTSDGAPICQGVIEK 5072
Qy 238 LELCSS-----ELLRLYRKGVVT-----EAEVKVYIQQLVGLHYLHS----- 277
Db 5073 REVGSTEWTKAAGNILDTHKRVTLGLTPKTYEYFVAAY-NAAGQGEYSVNSVPIITADNA 5131
Qy 278 -----HGVHLDI-----KPSNLMVHPAREDIKICDGPAGN-ITPAE-----LQFSQ 320
Db 5132 PTPRKINMGLTRDILAYAGERAKILVPFAASAPAKV-TFSKGENKISITPDPRKVEYS- 5189
Qy 321 YGSPFVSPRIIOQNVPVSEASDIWAMGVISYLSLTCSPPFAGSDRATLNLVLEGRVSW 380
Db 5190 ----DFLATLTIEK---SELTQ---GGLYFVELENSQ---GSDSASIRLKAVD---KPA 5232
Qy 381 SPMAHLSEDAKQFIKATLQRAQAPASAAQCLSH-----PW-----FLKSM 423
Db 5233 SPCHIRVEDIAPDC--CTLYMNPSSDGGSPFITNYIVEKILDLRHSQKWEKVSFVRLN 5290

1317 QY GTYTRFACVSKAGMPYSSPSEQVILGGPS-----HLASEEESQGRSAQ----- 1361
6180 Db QYEFRIITAEKNGHQSKCEPTAPVLIIPGDERKRRRGVDVEQGKIVRGKGVSVSNYDNY 6239
1362 QY -----PLP-----STKTFAQFIQIRGPRSVVRQWKEKASGALAAK-IIPYHP 1404
6240 Db VFDIWKYYPQVVEIKHDHVLHDYDIHEELGTGAFGVVHRVTERATGNNFAAFVMTPIHE 6299
1405 QY KDKTAVLREYALKGLRPHLAQLHAAYLSRPHLVILIELCSGPPELLCLA-ERASYSES 1463
6300 Db SKDEFVRKEIQTMSVLRHPTLVNLHDAFEDDNEMVMIYEFVSGSGELFSKVADENKMGSD 6359
1464 QY EVKDYLMWLSATQYIHNQHILHLDLRSENMIIT--EYNLLKVVLDLGNASLSQEKVLPS 1521
6360 Db EAVEVMRQVCKGLCHMHENNVVHLDLKPEINMFTTKRSNELKLIDFGLTAHLD-----PK 6414
1522 QY DKFK---DYLETMABELLEGQAVPQTDIWAIGVTAFIMLSNEYVPSSEGDARDLQGLRK 1578
6415 Db QSVKYTTGTBAFAAEVAGKPVGYITDMWSGVLSYILLSGLSFPGGENDDETUNNVKS 6474
1579 QY GLVRLSRC-----YAGLSGGAFAVLRSTLCAQWGRPCASSCLQCQPWLEEGPACSR 1630
6475 Db -----CDWNDDSAFSGISEDGKDFIRKULLADPNTRMTIHOALEHPWLT-PGNAPGR 6526
1631 QY PAPVTFPTAR 1640
6527 Db DSQI--PSSR 6534

RESULT 10
A35021
myosin-light-chain kinase (EC 2.7.1.117), skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 24-Sep-1999
C:Accession: A35021; A05120; A25830
R:Herring, B.P.; Stull, J.T.; Gallagher, P.J.
J. Biol. Chem. 265, 1724-1730, 1990
A:Title: Domain characterization of rabbit skeletal muscle myosin light chain ki
A:Reference number: A35021; UID:90110242; PMID:1688558
A:Accession: A35021
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-608 <HR>
A:Cross-references: GB:J05194; NID:g165505; PIDN:AAA31400.1; PID:g165506
R:Takio, K.; Blumenthal, D.K.; Edelman, A.M.; Walsh, K.A.; Krebs, E.G.; Titani,
Biochemistry 24, 6028-6037, 1985
A:Title: Amino acid sequence of an active fragment of rabbit skeletal muscle myoc
A:Reference number: A05120; UID:86104095; PMID:3841288
A:Accession: A05120
A:Molecule type: protein
A:Residues: 237-604 <TA>
R:Takio, K.; Blumenthal, D.K.; Walsh, K.A.; Titani, K.; Krebs, E.G.
Biochemistry 25, 8049-8057, 1986
A:Title: Amino acid sequence of rabbit skeletal muscle myosin light chain kinase
A:Reference number: A25830; UID:87101105; PMID:3542042
A:Accession: A25830
A:Molecule type: protein
A:Residues: 2-336/'K',337-604 <TA2>
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C:Keywords: ATP, muscle; phosphotransferase; serine/threonine-specific protein kinase
F:295-552/Domain: protein kinase homology <KIN>
F:303-311/Region: protein kinase ATP-binding motif

Query Match 5.3%; Score 465.5; DB 2; Length 608;
Best Local Similarity 29.2%; Pred. No. 2.1e-08;
Matches 131; Conservative 86; Mismatches 174; Indels 57; Gaps 13;

QY 43 LHSSLPALPGPPSMQVTTEDVQAQGGTGAQFEALIEGDP-----QPSVTMYKDSVQLVD 96
Db 157 LHS-----PSCPAITASTEKUPAQKPLSEASLIEFGVPATPGTPEGPAKAGGVDLIA 211
QY 97 STRLSQQQEG-----TTYSVLVRHVASKDAGVYITCLAQNTGGQVLC----- 137

Db 212 E---SKEAGEKAPQADQAKVQDTERGIFQAVPSE-----RPRPEVQALCLPAR 261
 Qy 138 KAEILLVGGDNEPSEKQSHR-----RKLHSFYEV--KEEIGRGVFGFKRVQHGKNGKI 189
 Db 262 BEDCFQILDDCPPPAPPAPPHRIVELRTGNTSVSBSMSKZALGGKGAGVCTCTEKSTGL 321
 Qy 190 LCAAKFTPLRG-RRTAQAYRERDILALSHPLVTGLDQFETKTLILILELCSSEELL 248
 Db 322 KLAARVTKQTPKQKEMVMLEIYVGNQNLNHNLIQLYAAIETPHEIYVLFMEYIEGGELFE 381
 Qy 249 RLYRKGV-VTEAEVKYVLIQQLVEGLHYLHSHGVHLHDIKPSNLMVHPAREDIKCDFFG 307
 Db 382 RIVEDYHLTEVDNWFVRQICDGLFHKVRVHLHDLPENILCVNTGHLVKLIIDFGL 441
 Qy 308 AONTTPAELQPSQVSGSPFVPEIQQNPVSEASDIWAMGVISYLSITCSPFAGESDRA 367
 Db 442 ARRYNPNEKLVNFTGPELSPVNVYDQISDKTDMSLGVITYMLLSGLSPFLGDDDTTE 501
 Qy 368 TLNVLEGRVSWSPMAHLSADAKFIKATLQAPQAPQAPSAACLSHPWFLKSPAEAA 427
 Db 502 TLNVLSGNWTFDEETFAVSDERAKDFVSNLIVKEQGRVSAACLSHPW-LNVL-NEKA 559
 Qy 428 HFINTK-----QLKFLARSRWORSLS 450
 Db 560 KRCNRRLKSQLLLKXVLMKRWKGNFIA 587
 RESULT 11
 S49128
 A:Description: Autophosphorylation of molluscan twitchin and interaction of its kinase d
 A:Reference number: S49128
 A:Accession: S49128
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-451 <HE1>
 A:Cross-references: EMBL:Z30161; NID:G509412; PIDN:CAA82911.1; PID:G509413
 R:Heierhorst, J.; Probst, W.C.; Vilim, F.S.; Buku, A.; Weiss, K.R.
 J. Biol. Chem. 269, 21086-21093, 1994
 A:Title: Autophosphorylation of molluscan twitchin and interaction of its kinase domain
 A:Reference number: A53923; MUID:94342273; PMID:8063728
 A:Accession: A53923
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 5-372 <HE2>
 A:Cross-references: GB:Z30161
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: ATP
 F:45-302/Domain: protein kinase homology <KIN>
 F:53-61/Region: protein kinase ATP-binding motif
 Query Match 5.3%; Score 463.5; DB 2; Length 451;
 Best Local Similarity 38.3%; Pred. No. 1.9e-08;
 Matches 105; Conservative 43; Mismatches 115; Indels 11; Gaps 4;
 Qy 149 EPDSKQSHRKLHSFYEVKEIGRGVFGFKRVQHGKNGKILCAAKFTIPLR-----PLRSRTFA 204
 Db 34 QPVEYKQG---SCDYDYDILELGGAGFVGRVRCVEKATGRVFEAKFTNPYPLDKYTL-- 88
 Qy 205 QAYRERDILALSHPLVTGLDQFETKTLILILELCSSEELLRLYRKGV-VTEARVYV 263
 Db 89 -VKNQETISINNQLHHPKLIINLHDAFEDKYDWMVLIIFLPSGGELFDRIAAEDYKMSAEVIN 147
 Qy 264 YIQQLVEGLHYLHSHGVHLHDIKPSNLMVHPAREDIKCDFFGFAQNTTPAELQPSQVGS 323
 Db 148 YMEQACEGLKHHHEHIVHLDIKPENIMCETKASVSKVLIIDFGLATKXNPDIIVKVTAT 207
 Qy 324 PFVSPPEIQQNPVSEASDIWAMGVISYLSITCSPFAGESDRA TLNVLEGRVSWSPSP 383

Db 208 AFAFAPEIVDRPVGDFYDMMWAGIVGLVLSGLSPFFAGEDDLETLQNVRCDNFEDEDA 267
 Qy 384 AAHLSEDAKFIKATLQAPQAPQAPSAACLSHPW 417
 Db 268 FSSVSPEAKDFIKLLQKEPRKRLTVHDALEHPW 301
 RESULT 12
 I37275
 A:Description: death-associated protein kinase (EC 2.7.1.1.) - human
 N:Alternate names: calmodulin-dependent protein kinase homology; DAP kinase
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 10-Jul-1998
 C:Accession: I37275; S39269
 C:Reiss, L.P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi, A.
 Genes Dev. 9, 15-30, 1995
 A:Title: Identification of a novel serine/threonine kinase and a novel 15-kD protein as]
 A:Reference number: A55614; MUID:95129831; PMID:78288949
 A:Accession: I37275
 A:Molecule type: mRNA
 A:Residues: 1-1423 <RES>
 A:Cross-references: EMBL:X76104; NID:G434846; PID:G434847
 C:Genetics:
 A:Gene: GDB:DAPK1; DAPK
 A:Cross-references: GDB:555932; OMIM:600831
 A:Map position: 9q34.1-9q34.1
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A:Pathway: apoptosis
 A:Note: activity is calmodulin dependent
 C:Superfamily: death-associated protein kinase; ankyrin repeat homology; protein kinase I
 C:Keywords: apoptosis; ATP; calmodulin binding; phosphotransferase; serine/threonine-spe
 F:11-267/Domain: protein kinase homology <KIN>
 F:13-27/Region: protein kinase ATP-binding motif
 F:285-308/Region: calmodulin binding #status Predicted
 F:370-402/Domain: ankyrin repeat homology <AN1>
 F:403-435/Domain: ankyrin repeat homology <AN2>
 F:436-468/Domain: ankyrin repeat homology <AN3>
 F:470-502/Domain: ankyrin repeat homology <AN4>
 F:503-535/Domain: ankyrin repeat homology <AN5>
 F:536-568/Domain: ankyrin repeat homology <AN6>
 F:569-601/Domain: ankyrin repeat homology <AN7>
 F:602-634/Domain: ankyrin repeat homology <AN8>
 F:642,64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted
 Query Match 5.2%; Score 456; DB 1; Length 1423;
 Best Local Similarity 33.1%; Pred. No. 9.3e-08;
 Matches 109; Conservative 65; Mismatches 119; Indels 36; Gaps 7;
 Qy 158 RKLLHSFYEVKEIGRGVFGFKRVQHGKNGKILCAAKFTIPLR-----SR---TRAQAYRER 210
 Db 6 QENVDDYDITGEEELSGQFAVVKCKREKSTGTQYPAKFIKGRKTSRRGVSEEDIEREV 65
 Qy 211 DILAALSHPLVTGLDQFETKTLILILELCSSEELLRLYRKGVVTAEARVYVLIQQLVE 270
 Db 66 SILKEICHNPVITLHEVYENKTDVILILELVAGGELFDLAEKESLTEBEATEFLKQILN 125
 Qy 271 GLHYLHSHGVHLHDIKPSNLMV--HPAREDIKCDFFGFA-QNITPAELQPSQVSGPEV 327
 Db 126 GVYLYLSLQTAHFDDLPENIMLLDRNVKPRIKIIDFGNEFKNI-----FGIPEFV 176
 Qy 328 SPETIQNPVSEASDIWAMGVISYLSITCSPFAGESDRA TLNVLEGRVSWSPMAHL 387
 Db 177 APVINYEPFGLADWMSIGVITYILLSGASPLGDTKQETLANVSAVNYEDEFVSNT 236
 Qy 388 SEDAKDPIKATLQAPQAPQAPSAACLSHPWF-----LKSMPAEAAHINTKQLKFLARSR 443
 Db 237 SALAKDFIRLLVKDPKGRMTIQDSLQHPWIKPQDTQALSRKASAVNMEKFKKFAARKK 296
 Qy 444 WQ-----RSLMSYKSLVMS 459
 Db 297 WKQSVRLISLCQLRSRSLRSNMSVARS 325

773 PFLGQPPAPAKASPPLDCKMGQDLSLPRPKPCSPSPGASQASSQVSSLRVGS 832
 720 STAG-PEGSAFC-----PGEIN--GKTIKTMSSSSSFDKSNLQC--SFRYKM 763
 833 SQVGTPEGPSLDAEGWTOEADLSDSTPLQPOQOVQTMKFKSLGGRGVAGVAGYGT-- 890
 764 S-----AEASKLQTLQESPLPVEQTKRVHVGVSTNGSGDSGQGTND 807
 891 FAFGGDAG--MLCQGPWARIAMVQSEEEQEEARAEQSEEEQEEARAE-- 941
 808 AKSNGDSRSEKKVLAQG-----SSSTDEGCETDQGNPDGASQESKSGNGSGSGN 857
 942 ----PLPQVSARPEVGVGRAPTRSSPEPTWEDIGQVSLVQIRDLSDGDAE-ADTISLDI 996
 858 ANGPTSHSSDLTLVGTASGQSKWRSYASSSSSGV-----LAGSAGSYSKLQNL 913
 997 SEVDPAYLNLSDLYDIKLPFEFMIFPKVPSAOPPEPPSPMAEELAEFPPTWFGEL 1056
 914 SR-GSKSNCSGPFYD-----SLDFAL-----PSGKSLPSCMGSSMLATPTPASASP-- 960
 1057 GPHAGLEITESEEDVDALLAEAAVGRKWKSSPSRSLFHFPRHLP----- 1102
 961 ---AGISSEHSE-----RSLYSHNSCHMEGA-LPLGLGLPQSSASTPT 1002
 1103 -----LDEPAELGLRERVKASVEHISRIKGRPEGLEKEGPRKPKPLGLASP 1148
 1003 PNPPTPPNGGVTFLDKRSPIHFREGRAS-----DGLVAQGLLSSGSLGTS 1050
 1149 RLSGLKSDRAPTF-----LRELSDETUV 1172
 1051 RVGVSVRYEQAKRHWGLIEIQLQLQQAQAAV 1081

RESULT 14
 JC7733
 death associated protein kinase related apoptosis inducing protein kinase 2 homolog, DRJ
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 14-Dec-2001
 C;Accession: JC7733; PC7178
 R;Matumoto, M.; Miyake, Y.; Nagita, M.; Inoue, H.; Shitakubo, D.; Takemoto, K.; Ohtsuka
 J. Biochem. 130, 217-225, 2001
 A;Title: A serine/threonine kinase which causes apoptosis-like cell death interacts with
 A;Reference number: JC7733; MUID:21374135; PMID:11481038
 A;Contents: Brain
 A;Accession: JC7733
 A;Molecule type: mRNA
 A;Residues: 1-371 <MAT>
 A;Accession: PC7178
 A;Molecule type: protein
 A;Residues: 227-371 <MA2>
 C;Comment: This kinase, a novel calcineurin homologous protein (CHP) binding protein wit
 involved in the transfer of Na+/H+ exchanger 1 process and in some apoptotic events.
 C;Genetic:
 A;Gene: drak2
 C;Keywords: apoptosis

Query Match 5.2%; Score 451; DB 2; Length 371;
 Best Local Similarity 35.2%; Pred. No. 4e-08;
 Matches 106; Conservative 68; Mismatches 111; Indels 16; Gaps 7;

QY 162 HSFYEV-KEETGRGVGVKRVQHKNGKILCAAKFIPLSR---TRAQVREDDIL-AAL 216
 DB 29 NNFTLTPELGRGKFAVVRQICISKSTQGEYAAKFLKRRRGQDCRAEILFEAVLELAR 88
 QY 217 SHPLVTGLDDQFETKTLILILELCSSEELDLRYK--GVWTEAEVKVVIQQLVEGLHY 274
 DB 89 SCPHVNLHEVYEYATEIILVLYAAGEIFNLCLPELAEMVSENDVIRLIKQILEGVHY 148
 QY 275 LSHGVHLHDKPSNLM--VHPAREDIKICDFQAFQNIITPAELOFSQYSGSPFVSPBEII 332
 DB 149 LHQNNIVHLDLKPNQILLISYIPL-GDIKIVDFGMSRKIGNAGSELREIMGTPTSYLAPEIL 207

116 VASKDAGVYICLQNTGGV---PLRSRTAQAYRERDILAAALSHPLVTLGLDQFE 229
 90 VACKDALLAQKLFASGGSGTPGSPSTSSAVAGGIGSGKDLLKLBPMRV-GFYDIERTIG 148
 173 RGVEFGVYKRVQKGNKILCAKEFI---PLRSRTAQAYRERDILAAALSHPLVTLGLDQFE 229
 149 KGNFAVVKLARHRTKNEVAIKIDKSLDQTNLQVYREVEIMKRLKHPHIIKLYQWVE 208
 230 TRKTLIILILCSSEELLRLYKGVVTEAEVKVYIQLVGLHYLHSHGVHLHDIKPSN 289
 209 TKMIIYVSEVAGGEIFDIYAKIRGMSAARFKFWQIISAVYCHKKGIHVHREDLKAEN 268
 290 ILMVHPAREDIKICDFGAQNIIPABLOFSQVSGSPFVSPFIIQ-QNPFVSEASDIWAMGV 348
 269 LLL--DLNMNIKIADFGSNHFKPGELLATWCQSPPYAAPFVEGKQYTGPEIDWLSGV 326
 349 ISYLSLTCSPFAGESDRATLLNVLEGRVSWSPMAAHLSEDAKDFIKATLCRAPQAPS 408
 327 VLYVLCVGAUFPDQSTLQSLRDLRVLSGRFR---IPFFMSSECHLIRMLVLETRRYT 382
 409 AAQCLSHPWFLKSM-----PAEE-----AHFINTKQLKFLARS 443
 383 IDQIKRHWMCPELLEHVLIAKYNLGAERQTSVEPSEDILRMAEYVVGIGSDK---TRAS 439
 444 WQSLMSYKILVWRSIPPELLRGPDPSPSLGVARHLCRDTGGSSSSSS-----SSDELAP 499
 440 LKNTYDTHVAATYLLQDRVSHKKEQSNGLGAS-----ALASSTASGRMIYSSRNDHQ 493
 500 F-----ARAKSLPPSPVTHSPHLPGRFLRPSASLPFEAEASERSTEAPAPASPE-GAG 553
 494 TQOQSQQQSKTISTSSILAKDQCHKR-----LSRHQTVLMSERNAHAGATPTVPDPGFG 547
 554 PPAQOQ-----CVPRHVSIRSLFYHQAGESPEHGNALPGSRHARRHLLKGYIAGA 607
 548 YKAYGQLPLPLTGHSS-----HLTG-----YINGGGVEVD 579
 608 LPGLREPLMBHRYLEBEAAREOATLLAKAPFETALRLPASGTHLAPCHSHLSHSDSPS 667
 580 ASGIPLP-MRYTEL-----PTAASPAPS-----NCSSTSSRVGR-HSLSSSSPR 621
 668 TPRP-----SSBACAEQRLPSAPSGGAPIRDGMCHPGQSKQLPSTGGHPOTA 714
 622 SHRPVALSLDNNPNSLANLRCEWME-----AGGPFVGAUVPLASKQLHQT----- 669
 715 QPERSPDPSWGOAPFCHP--KQGSAPQGGCSPHPAVAPCPGPGSPGSCKEAPLPVSS 772
 670 -----ISEFTIKQSTEDCRALLQOSTAVAEG-KDDPPKAESSVGVGVP-----PASTTPTS 719

Query Match 5.2%; Score 454.5; DB 2; Length 1398;
 Best Local Similarity 22.4%; Pred. No. 1e-07;
 Matches 262; Conservative 149; Mismatches 467; Indels 293; Gaps 47;

QY 116 VASKDAGVYICLQNTGGV---PLRSRTAQAYRERDILAAALSHPLVTLGLDQFE 229
 DB 90 VACKDALLAQKLFASGGSGTPGSPSTSSAVAGGIGSGKDLLKLBPMRV-GFYDIERTIG 148
 QY 173 RGVEFGVYKRVQKGNKILCAKEFI---PLRSRTAQAYRERDILAAALSHPLVTLGLDQFE 229
 DB 149 KGNFAVVKLARHRTKNEVAIKIDKSLDQTNLQVYREVEIMKRLKHPHIIKLYQWVE 208
 QY 230 TRKTLIILILCSSEELLRLYKGVVTEAEVKVYIQLVGLHYLHSHGVHLHDIKPSN 289
 DB 209 TKMIIYVSEVAGGEIFDIYAKIRGMSAARFKFWQIISAVYCHKKGIHVHREDLKAEN 268
 QY 290 ILMVHPAREDIKICDFGAQNIIPABLOFSQVSGSPFVSPFIIQ-QNPFVSEASDIWAMGV 348
 DB 269 LLL--DLNMNIKIADFGSNHFKPGELLATWCQSPPYAAPFVEGKQYTGPEIDWLSGV 326
 QY 349 ISYLSLTCSPFAGESDRATLLNVLEGRVSWSPMAAHLSEDAKDFIKATLCRAPQAPS 408
 DB 327 VLYVLCVGAUFPDQSTLQSLRDLRVLSGRFR---IPFFMSSECHLIRMLVLETRRYT 382
 QY 409 AAQCLSHPWFLKSM-----PAEE-----AHFINTKQLKFLARS 443
 DB 383 IDQIKRHWMCPELLEHVLIAKYNLGAERQTSVEPSEDILRMAEYVVGIGSDK---TRAS 439
 QY 444 WQSLMSYKILVWRSIPPELLRGPDPSPSLGVARHLCRDTGGSSSSSS-----SSDELAP 499
 DB 440 LKNTYDTHVAATYLLQDRVSHKKEQSNGLGAS-----ALASSTASGRMIYSSRNDHQ 493
 QY 500 F-----ARAKSLPPSPVTHSPHLPGRFLRPSASLPFEAEASERSTEAPAPASPE-GAG 553
 DB 494 TQOQSQQQSKTISTSSILAKDQCHKR-----LSRHQTVLMSERNAHAGATPTVPDPGFG 547
 QY 554 PPAQOQ-----CVPRHVSIRSLFYHQAGESPEHGNALPGSRHARRHLLKGYIAGA 607
 DB 548 YKAYGQLPLPLTGHSS-----HLTG-----YINGGGVEVD 579
 QY 608 LPGLREPLMBHRYLEBEAAREOATLLAKAPFETALRLPASGTHLAPCHSHLSHSDSPS 667
 DB 580 ASGIPLP-MRYTEL-----PTAASPAPS-----NCSSTSSRVGR-HSLSSSSPR 621
 QY 668 TPRP-----SSBACAEQRLPSAPSGGAPIRDGMCHPGQSKQLPSTGGHPOTA 714
 DB 622 SHRPVALSLDNNPNSLANLRCEWME-----AGGPFVGAUVPLASKQLHQT----- 669
 QY 715 QPERSPDPSWGOAPFCHP--KQGSAPQGGCSPHPAVAPCPGPGSPGSCKEAPLPVSS 772
 DB 670 -----ISEFTIKQSTEDCRALLQOSTAVAEG-KDDPPKAESSVGVGVP-----PASTTPTS 719

QY 333 QONFVSEASDIWAMGVISYLSLTCSPPFAGESDRATLNLVLEGRVSWSSPMAHLSEDAK 392
Db 208 NYDITATDNWNIIGIAYMLLTHTSFVGEDNQETVLINISQVNDVSEEMFSSVQLAT 267
QY 393 DFKATLQAPQAPSAQCLSHWFLK-----SMPAEHAHINTKQLKFLARSWOR 446
Db 268 DFIQSLVKNPEKPTAESCLSHSWLQWDGSLFHPETSESSOTQDLSRSEDKTPK 327
QY 447 S 447
Db 328 S 328

RESULT 15
A28798
myosin-light-chain kinase (EC 2.7.1.117), skeletal muscle - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jan-1989 #sequence_revision 12-Jan-1989 #text_change 19-Dec-1997
C:Accession: A28798; A60441
R:Roush, C.L.; Kennelly, P.J.; Glaccum, M.B.; Helfman, D.M.; Scott, J.D.; Krebs, E.G.
J. Biol. Chem. 263, 10510-10516, 1988
A:Title: Isolation of the cDNA encoding rat skeletal muscle myosin light chain kinase. S
A:Reference number: A28798; MUID:88273159; PMID:2839493
A:Accession: A28798
A:Molecule type: mRNA
A:Residues: 1-610 <ROU>
A:Cross-references: GB:J03886
R:Herring, B.P.; Nunnally, M.H.; Gallagher, P.J.; Stull, J.T.
Am. J. Physiol. 256, C399-C404, 1989
A:Title: Molecular characterization of rat skeletal muscle myosin light chain kinase.
A:Reference number: A60441; MUID:89148435; PMID:2465691
A:Accession: A60441
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 296-610 <HER>
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; calmodulin binding; muscle; phosphotransferase; serine/threonine-speci
F:297-554/Domain: protein kinase homology <KIN>
F:305-313/Region: protein kinase ATP-binding motif

Query Match 5.1%; Score 450; DB 2; Length 610;
Best Local Similarity 28.9%; Pred. NO. 6.7e-08;
Matches 128; Conservative 85; Mismatches 178; Indels 52; Gaps 14;

QY 43 LHS-SLPALGPPSQVIEDVQATGCTAQFEALIEG-----DPQPS-----VTWY 88
Db 164 LHSRSPALISCEKTLAKPLSETT-----ELIFAGVSETPDPDPGPAKDEGGTNTL 217
QY 89 KDSVLVDSTRLSQQ--QEGTYSVLVRHVASKDAGVVTCLAQNTGGQVLC-----KAEEL 142
Db 218 ADGKEAEAGAEQAKVQDTSQRIGFQAVPSRAEV-----GOALCLTAKEEDCF 268
QY 143 VLGGNEPDPSEKQSHR-----RKLHSFEV--KEEIGRGVGVKRVQHKGNKILCAAK 194
Db 269 QILDDCPPPPAPFPHRIVELRTGNVSSEFSMNSKEALGGKFGAVCTCTERSTGKLAAK 328
QY 195 FIPLRS-RTRAQAYRERDILALSHPLVTGLLDQFETKTLILILELCSSEELDLRYK 253
Db 329 VIKQTPKDKEMVLLIEVWQNLHNLQLYSATSESHIILFWEYIEGGELPERIVDE 388
QY 254 GV-VTAEVKVVIQQLVEGLVHLHSHGVHLHDIKPSNLMVHPAREDIKICDFGAQNI 312
Db 389 DYOLTEVDTMVFVRQICDGLFMKRVHLHLKPNELCVNTTGHVLIKIDFGLARRYN 448
QY 313 PAELQFSQVGSPEFVSPEIQQNPVSEASDIWAMGVISYLSLTCSPPFAGESDRATLNV 372
Db 449 PNEKLVNFGTPEFLSFEVNVYDQISDKTDMNSLGLVITYMLLSGLSPFLGDDDDTETLNV 508
QY 373 LEGRVSWSSPMAHLSEDAKDFKATLQAPQAPSAQCLSHWFLKSPAEHAHINT 432
Db 509 LSAWYFDEETPEAVSEDAKDFVSNLITKDQARMSAEQCLAHFW-LNNL-AEKARCRN 566
QY 433 K-----QLKFLARSRWQRSLMS 450

Db 567 RLKSOILLKKYLMKRWKCNFIA 589
Search completed: April 23, 2004, 15:11:34
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 14:55:57 ; Search time 24 Seconds
(without alignments)

3612.367 Million cell updates/sec

Title: US-10-697-263-2

Perfect score: 8740

Sequence: 1 MGCCRLGGCGSVAHVSQG.....RNREKRALLYKRNHLAQVR 1665

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	592.5	6.8	3038	1	TRIO HUMAN
2	550.5	6.3	1176	1	KMLS BOVIN
3	544.5	6.2	1147	1	KMLS RABIT
4	541.5	6.2	1914	1	KMLS HUMAN
5	532.5	6.1	1906	1	KMLS CHICK
6	489.5	5.6	448	1	DAK3 MOUSE
7	489.5	5.6	448	1	DAK3 RAT
8	475.5	5.4	370	1	DAK2 MOUSE
9	471.5	5.4	1432	1	DAK1 HUMAN
10	469.5	5.4	1442	1	DAK1 MOUSE
11	468.5	5.4	535	1	KML2 HUMAN
12	466.5	5.3	454	1	DAK3 HUMAN
13	465.5	5.3	370	1	DAK2 HUMAN
14	465.5	5.3	607	1	KML2 RABIT
15	463.5	5.3	1050	1	ULK1 HUMAN
16	460.5	5.3	438	1	KMLS SHEEP
17	451.5	5.2	371	1	S17B RAT
18	450.5	5.1	609	1	KML2 RAT
19	449.5	5.1	1051	1	ULK1 MOUSE
20	447.5	5.1	397	1	S17A RABIT
21	445.5	5.1	414	1	S17A HUMAN
22	441.5	5.1	374	1	KCCI RAT
23	440.5	5.0	424	1	KPSH HUMAN
24	438.5	5.0	372	1	S17B MOUSE
25	437.5	5.0	374	1	KCCI MOUSE
26	431.5	4.9	794	1	KILL HUMAN
27	428.5	4.9	372	1	S17B HUMAN
28	427.5	4.9	370	1	KCCI HUMAN
29	418.5	4.8	414	1	KCCI EMENI
30	413.5	4.7	779	1	SNIL MOUSE
31	412.5	4.7	752	1	VRKA HUMAN
32	406.5	4.6	602	1	CRK DAUCA
33	405.5	4.6	776	1	SNIL RAT

34 404.5 4.6 469 1 KCC4 MOUSE
35 404.5 4.6 786 1 SNIL HUMAN
36 399.5 4.6 473 1 KCC4 HUMAN
37 390.5 4.5 664 1 KCCB HUMAN
38 389.5 4.5 474 1 KCC4 RAT
39 389.5 4.5 240 1 KML2 MOUSE
40 387.5 4.4 733 1 K6A2 MOUSE
41 387.5 4.4 740 1 K6A3 HUMAN
42 387.5 4.4 740 1 K6A3 MOUSE
43 385.5 4.4 752 1 K6A1 CHICK
44 384.5 4.4 774 1 MRK2 MOUSE
45 384.5 4.4 735 1 K6A1 RAT

ALIGNMENTS

RESULT 1
TRIO HUMAN
ID TRIO HUMAN STANDARD; PRT; 3038 AA.
AC 075962; Q13458;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Triple functional domain protein (TPPRF interacting protein).
GN TRIO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fibroblast;
RX MEDLINE=96224308; PubMed=8643598;
RA Debant A., Serra-Pages C., Seipel K., O'Brien S., Tang M., Park S.-H.,
RA Streuli M.;
RT "The multidomain protein Trio binds the LAR transmembrane tyrosine
RT phosphatase, contains a protein kinase domain, and has separate rac-
RT specific and rho-specific guanine nucleotide exchange factor
RT domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5466-5471(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Streuli M.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP STRUCTURE BY NMR OF 1227-1407 AND MUTAGENESIS.
RX MEDLINE=99003194; PubMed=9790533;
RA Liu X., Wang H., Eberstadt M., Schnuchel A., Olejniczak E.T.,
RA Meadows R.P., Schkeryantz J.M., Janowick D.A., Harlan J.E.,
RA Harris E.A.S., Staunton D.E., Fesik S.W.;
RT "NMR structure and mutagenesis of the N-terminal Dbl homology domain
RT of the nucleotide exchange factor Trio.";
RL Cell 95:269-277(1998).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99276567; PubMed=10341202;
RA Seipel K., Medley Q.G., Kedarsha N.L., Zhang X.A., O'Brien S.P.,
RA Serra-Pages C., Hemler M.E., Streuli M.;
RT "Trio amino-terminal guanine nucleotide exchange factor domain
RT expression promotes actin cytoskeleton reorganization, cell migration
RT and anchorage-independent cell growth.";
RL J. Cell Sci. 112:1825-1834(1999).
CC -!- FUNCTION: PROMOTES THE EXCHANGE OF GDP BY GTP. TOGETHER WITH
CC LEUCOCYTE ANTIGEN-RELATED (LAR) PROTEIN, IT COULD PLAY A ROLE IN
CC COORDINATING CELL-MATRIX AND CYTOSKELETAL REARRANGEMENTS NECESSARY
CC FOR CELL MIGRATION AND CELL GROWTH.
CC -!- SUBUNIT: INTERACTS TO FORM A COMPLEX WITH LEUCOCYTE ANTIGEN
CC -!- RELATED PROTEIN.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=075962-1; Sequence=Displayed;

FT	REPEAT	252	359	SPECTRIN 1.
FT	REPEAT	479	585	SPECTRIN 2.
FT	REPEAT	819	925	SPECTRIN 3.
FT	REPEAT	1050	1157	SPECTRIN 4.
FT	DOMAIN	1233	1408	DH 1.
FT	DOMAIN	1421	1532	PH 1.
FT	DOMAIN	1597	1653	SH3.
FT	DOMAIN	1910	2086	DH 2.
FT	DOMAIN	2038	2212	PH 2.
FT	DOMAIN	2626	2716	IG-LIKE C2-TYPE.
FT	DOMAIN	2737	2993	PROTEIN KINASE.
FT	DOMAIN	656	659	POLY-GLN.
FT	DOMAIN	1786	1791	POLY-SER.
FT	DOMAIN	2233	2263	POLY-GLY.
FT	DOMAIN	2486	2492	POTENTIAL.
FT	DISULFID	2637	2700	ATP (BY SIMILARITY).
FT	NP BIND	2743	2751	ATP (BY SIMILARITY).
FT	BINDING	2766	2766	BY SIMILARITY.
FT	ACT SITE	2856	2856	PSVGHPPVTVSSAASSQAEADKWS -> AAAGVGAAAA
FT	VARSPLIC	2242	2308	GPVAANAATAAPAAAAPPAPGAGAPPGSPSLSDTTPPCW
FT				/Frid=VSP_004467.
FT	VARSPLIC	2309	3038	Missing (in isoform 2).
FT	MUTAGEN	1240	1240	/Frid=VSP_004468.
FT	MUTAGEN	1244	1244	E-A>-A: 50% DECREASE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1330	1330	T-A>-A: 40% DECREASE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1367	1367	N-A>-A: NO CHANGE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1368	1368	V-A>-A: 90% DECREASE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1369	1369	Q-A>-A: 80% DECREASE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1371	1371	R-A>-A: 80% DECREASE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1372	1372	T-A>-A: 80% DECREASE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1375	1375	K-A>-A: LOSS OF NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1378	1378	L-A>-A: 40% DECREASE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	MUTAGEN	1379	1379	K-A>-A: NO CHANGE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT	SEQUENCE	3038 AA;	341611 MW;	E-A>-A: 30% DECREASE IN NUCLEOTIDE EXCHANGE ACTIVITY.
FT				28620F3B513EB74B CR64;
Query Match		6.8%;	Score 592.5;	
Best Local Similarity		34.5%;	Fred. No. 1.9e-13;	
Matches 145;	Conservative	69;	Mismatches 191;	Indels 15; Gaps 6;
QY	53	PPSQVTVIEDVQAQTGTGAQFEALIGDQPDPVTWKDSVLQVD-----STRLSQQCEGT	107	
Db	2625	PFPEVIPLSEVTCBTGETVVLRCVCGRKASITWKGPENHTLNDGHYSISYSDLGEAT	2684	
QY	108	TYSVLVRHVAKDAGVYTCLAQNTGGQVLCRAELLVLCGDNEPSEKQSRRKLHSFYEV	167	
Db	2685	---LKIVGVTTEDDGTYTICIANVDMSGSSASSLRVLGFG--MDGMVMTWKDNPDFSYSE	2739	
QY	168	KEBIGRGVGFVKRVQHKNGKILCAAKFIPLRSRTFAQYRERDILAALSHPLVTGLDQ	227	
Db	2740	VAELGRGRFSVVKKCDQKGTKRAVATKFVNKKLMKRQDVTHELGILOSQHPLLVLGLDT	2799	
QY	228	PETRKYLILLILCSSEEMDLRLYKGVVTEAVKNVYIQQQLVEGVHLHSHGVHLHDIKP	287	
Db	2800	FETTSVILVENADQGRLLCCVWRWGSLTEGKRAHLGVLEVLEARVRLHNCRATHLDLKP	2859	
QY	288	SNILMVHP-AREDIKICDFGFAQNITPAELOFSQVGSPEFVSPIIIQQNPVSEASOITWM	346	
Db	2860	ENLVDESIAKPTIKLATGDDVOLNTTYYIHOLLGNPEFAAPTIIILGNPVISTSTWSV	2919	

QY 347 GVSYLSLTCSPPAGESDRATLNLVLEGRVSNWSPMAHLSEDAKDFIKATLQAPQAR 406
Db 2920 GVITVLSGVSFPDLDVEETCTNCRLOFDFPDYFKGVGOKAKFVCLLQEDPAKR 2979
QY 407 PSAAQCLSHPWFLKSMFAEEAHFINTKQLKFLIARSRWQ---RSLMSYKSLVWRISPL 463
Db 2980 PSAAALQEQW-LQAGNGRSTGVLDTSRLTSFTIERRHONDVPIRSIKNQLSRLLPV 3038
RESULT 2
KMLS_BOVIN
ID KMLS_BOVIN STANDARD; PRT; 1176 AA.
AC Q28824;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
DE [Contains: Telokin].
GN MILK.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=92203148; PubMed=1284247;
RA Kobayashi H., Inoue A., Mikawa T., Kuwayama H., Hotta Y., Masaki T.,
RA Ebashi S.;
RT "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting
RT myosin light chain kinase activity.";
RL J. Biochem. 112:786-791(1992).
CC -!- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
CC SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
CC IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT
CC FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
CC -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
CC light-chain] phosphate.
CC -!- SUBUNIT: ISOFORM TELOKIN BINDS CALMODULIN.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=At least 3 isoforms, Non-muscle, Smooth-muscle (shown
CC here) and Telokin, are produced by alternative initiation.
CC Isoform Non-muscle is the longest and telokin is a C-terminal
CC section without catalytic activity;
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S57131; JAB25794.1; -,
CC PIR; JN0583; JN0583.
CC HSSP; P56276; 1TLK.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003962; FNIII subd.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig-c2.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00041; fn3; 1.
CC Pfam; PF00047; ig; 2.
CC Pfam; PF00069; pkinase; 1.

PRINTS; PR00014; FNTYPEIII.
PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; IG2; 2.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_SI; 1.
KW transferase; Serine/threonine-protein kinase, Calmodulin-binding;
KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW Alternative initiation.
FT CHAIN 1 1176
FT MYOSIN LIGHT CHAIN KINASE, ISOFORM
FT SMOOTH-MUSCLE.
FT MYOSIN LIGHT CHAIN KINASE, ISOFORM
FT TELOKIN.
FT FOR ISOFORM TELOKIN.
FT 16 X 12 AA TANDEM REPEATS.
FT 1.
FT 2.
FT 3 (INCOMPLETE).
FT 4.
FT 5.
FT 6.
FT 7.
FT 8.
FT 9.
FT 10.
FT 11.
FT 12.
FT 13.
FT 14.
FT 15.
FT 16.
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT FIBRONECTIN TYPE-III.
FT PROTEIN KINASE.
FT CALMODULIN-BINDING.
FT IG-LIKE C2-TYPE 3.
FT ATP (BY SIMILARITY).
FT ATP (BY SIMILARITY).
FT BY SIMILARITY.
FT POLY-GLU.
SQ SEQUENCE 1176 AA; 128824 MW; F53DC6D4D42D4B97 CRC64;
Query Match 6.3%; Score 550.5; DB 1; Length 1176;
Best Local Similarity 25.3%; Pred. No. 2.1e-12;
Matches 145; Conservative 91; Mismatches 191; Indels 147; Gaps 10;
Qy 45 SSLPALPG-----PPSMQVTIEDVQQTGTAQPEAIIIGDPQP 83
Db 468 SSLPVLGTS DATVKKPAPKTPPKAAMPQIIQFPDQKVRAGESVELFKVAGTQPI 527
Qy 84 SVTWYKDSVQLVDSRLSQQEGTYSILVRHVASKDAGVYTCLAQN----- 130
Db 528 TCTWMKFRKQIQDSEHIKYVENSEQSKLTIRAAOEHCGCYTLAVENKLGSRQAQVNLTV 587
Qy 131 -----TGGQVL-----CK-- 138
Db 588 VKPDPPAGTFCASDIRSSSLTSLWSYSGSDGSAVSYSVIMDSVDKTKWELATCRST 647
Qy 139 -----AELLVLG--GDNEP-----DSEKQ-- 155
Db 648 SFNVQDLLPDREYKFRVRAINVVGTSPEQSELTALGEKPEEPKDEVEVSDDEKPE 707
Qy 156 -----SHRKLHSGFYEVKEEIGRGVGFVKRVQHKNGKILCAKFIPLRSRTRQAY 207
Db 708 VDRVTVTNTQKVSDFYDIERLGGKFGQVFLRVLEKTKTKINWAGKFKVAYSKEKENI 767
Qy 208 R-ERDILAALSHPLVTGLDQFETRTKLILILELCSSEBLLDRLYRKGV-VTEAEVKVYI 265
Db 768 RQISIMNCLHHPKLVQCVDAFEERANIWMVLEIVSGGELPERIIDEDELFELTERSCIKYM 827

QY 266 QQLVEGLHYLHSHGVLDLTKPSNLMVHPARSDIKICDFGFAONTTPAELQFSQVGSPE 325
 DB 828 KOISGEVYTHKQIVHLDLKPENIMCVNKTGRILKIDFGLARRLENAGSLKVLFGTPE 887
 QY 326 FVSEIITQONPVSEASDIWANGVTSYLSLTCSSPEAGESDRATLLNLVLEGRVSWSSPMAA 385
 DB 888 FVAREVINYEIGVATDWSIGVICILVSLGSPFNGDNDNETLANVTATWDFDEAPD 947
 QY 386 HLSDAKDFKATLQAPQAPRPAAGAACLSHPFLKMPAEBAHFINTKOLKELLARSQW 445
 DB 948 EISDAKDFISNLKDKMKRLNCTQLOHFWLMDKTKMEAKKLSKDRMKKYMARRKWQ 1007
 QY 446 RSLMSYKSLVMSRISPEL-----LRGPPDSP 471
 DB 1008 KTGNAVRAIGLSLMSVAMISGLSGKSGTSGTSP 1041

RESULT 3
 ID XMLS RABBIT STANDARD; PRT; 1147 AA.
 AC P2294; Q28729;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)
 DE [Contains: Telokin].
 GN MYLK.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Smooth muscle;
 RX MEDLINE=92084694; PubMed=1748666;
 RA Gallagher P.J., Herring B.P., Griffin S.A., Stull J.T.;
 RT "The carboxyl terminus of the smooth muscle myosin light chain kinase
 is expressed as an independent protein, telokin.";
 RL J. Biol. Chem. 266:23945-23952(1991).
 RN [2]
 RP SEQUENCE OF 993-1147 FROM N.A. (TELOKIN).
 RX MEDLINE=92084695; PubMed=1748667;
 RA Gallagher P.J., Herring B.P.;
 RT "The carboxyl terminus of the smooth muscle myosin light chain kinase
 is expressed as an independent protein, telokin.";
 RL J. Biol. Chem. 266:23945-23952(1991).
 CC -!- FUNCTION: Phosphorylates a specific serine in the N-terminus of a
 CC myosin light chain.
 CC -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
 CC light-chain] phosphate.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=At least 3 isoforms, Non-muscle, Smooth-muscle (shown
 CC here) and Telokin, are produced by alternative initiation.
 CC Telokin is a C-terminal section with no catalytic activity;
 CC -!- DOMAIN: TELOKIN BINDS CALMODULIN.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -----
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 CC -----
 CC EMBL; M76233; AAA31408.1; -;
 CC EMBL; M76234; AAA31408.1; -;
 CC EMBL; M76181; AAA31409.1; -;
 CC PIR; A41675; A41675.

PIR; A59307; A59307.
 HSP; P56276; ITLK.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003962; FN III subd.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG-c2.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00047; ig; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00014; FNTYPELII.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00835; IG LIKE; 3.
 DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS0011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS0108; PROTEIN KINASE-ST; 1.
 DR Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
 KW Alternative initiation.
 FT CHAIN 1 1147
 FT MYOSIN LIGHT CHAIN KINASE, ISOFORM
 FT SMOOTH-MUSCLE.
 FT MYOSIN LIGHT CHAIN KINASE, ISOFORM
 FT TELOKIN.
 FT FOR ISOFORM TELOKIN.
 FT 16 X 12 AA TANDEM REPEATS.
 FT 1.
 FT 2.
 FT 3 (INCOMPLETE).
 FT 4.
 FT 5.
 FT 6.
 FT 7.
 FT 8.
 FT 9.
 FT 10.
 FT 11.
 FT 12.
 FT 13.
 FT 14.
 FT 15.
 FT 16.
 FT IG-LIKE C2-TYPE 1.
 FT IG-LIKE C2-TYPE 2.
 FT FIBRONECTIN TYPE-III.
 FT PROTEIN KINASE.
 FT CALMODULIN-BINDING.
 FT IG-LIKE C2-TYPE 3.
 FT ATP (BY SIMILARITY).
 FT ATP (BY SIMILARITY).
 FT BY SIMILARITY.
 FT POLY-GLU.
 FT C -> R (IN REP. 2).
 SQ SEQUENCE 1147 AA; 125719 MW; F0395624C6531024 CRC64;

Query Match 6.2%; Score 544.5; DB 1; Length 1147;
 Best Local Similarity 23.7%; Pred. No. 3.3e-12;
 Matches 149; Conservative 97; Mismatches 206; Indels 177; Gaps 10;
 QY 48 PALPPSPMOVIEDVQAGTGTGTAQFAEAIIGDPPQSVTVYKDSVQLVDSRLSQQEGT 107
 DB 463 PRAATPPQIPQPPDEQKVRAGERVELFGKVAGTQPICTWKKFKQIQDSEHIKENSEA 522
 QY 108 TVSLVLRHVASKDAGVYTCLAQNTGGQVLCXAELLVLG----- 145
 DB 523 GSKLTILAAQHQHCQCYLLVENKLGSQAQVNLTVVDKPDFFAGTFCASDIRSSITLS 582
 QY 146 -----G 146

Db 583 WYSSYDGGSAVOSYSVEIWDSDVDMWTELATCRSTSFNVRDILLDPREKFKVRRAINYG 642
 QY 147 DNEP-----DSEKQ-----SHRRKLHSFYEVKEEI 171
 Db 643 TSFSPQSELTUVEKEPEKONVEVSDDEKEPEVDYRTVTNATEQKVSDFYDIERL 702
 QY 172 GRGVGFVKRVQHGKNGKILCAAKFIPLRSRTAQAAYRERD-----ILALSHPLVTGL 224
 Db 703 GSKGFGVFLVEKTKGWAGKFF-----KAYSAREKENIPAEIGIMNCLHHPKLVQC 756
 QY 225 LDOPEFRKTLILILELCSSEELDLRYRGV-VTEAEVQVYIQOVLVEGLYHLSHGVLHL 283
 Db 757 VDAFEKANKVMVLEIVSGELFERIDFELTERECIKYMRQISEGVYIHKOGIVHL 816
 QY 284 DIRPSNLMVHPAREDIKIDCFQAGNITPAELQFSQYSPFVSPPEIQQNPVSEASDI 343
 Db 817 DLKPEIMCVKNGTKRIKIDFGLARLENAGSLKVLFGTPEFVAPVINEPIYSYADM 876
 QY 344 WAGVITSYLSLTCSSPAGESDRAILLNVLGRVSWSSPMAHLSEDAKDTKATLQAP 403
 Db 877 WSGVTCYILVSLGSLSPFGNDNETLANVTSATWDFDFAFEISDDAKDFISNLLKDM 936
 QY 404 QARPSAAQCLSHFWFLKSPAEAHFINTKQLKFLARSRMORSLSYKSLVMSRISPEL 463
 Db 937 KRLDCTQCLQHPWLMKDTKNWEAKLSKDRMKYMARKKQKTGNVAVRAIGRLSSMAMI 996
 QY 464 LRGPDPSPSLGVARHLCRDTGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 523
 Db 997 -----SGLSGKSGSTGS-----PTSPLT----- 1014
 QY 524 RPSASLPEAEASERSTEAPA---PPASP 549
 Db 1015 --AERLETEDEVQAFLEAVEKPHVKP 1041

RESULT 4

KOLLS HUMAN
 ID KOLLS HUMAN STANDARD; PRT; 1914 AA.
 AC Q15746; Q95796; Q95797; Q95798; Q95799; Q14844; Q16794; Q9UBG5;
 AC Q9UIT9;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Myosin light chain kinase, smooth muscle and non-muscle isoforms
 DE (EC 2.7.1.117) (MLCK) [Contains: telokin (Kinase related protein)
 DE (KRP)].
 GN MYLK OR MLCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=97304466; PubMed=9160829;
 RA Garcia J.G.N., Lazar V.L., Gilbert-Mcclain L.I., Gallagher P.J.,
 RA Verin A.D.;
 RT "Myosin light chain kinase in endothelium: molecular cloning and
 RT regulation.";
 RL Am. J. Respir. Cell Mol. Biol. 16:489-494 (1997).
 RN [2]
 RN REVISIONS.
 RA Brukov K.G., Garcia J.G.N.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORMS 2; 3A; 3B AND 4).
 RC TISSUE=Umbilical vein;
 RX MEDLINE=99216419; PubMed=10198165;
 RA Lazar V.L., Garcia J.G.N.;
 RT "A single human myosin light chain kinase gene (MLCK; MYLK).";
 RL Genomics 57:256-267 (1999).
 RN [4]

RP REVISIONS (ISOFORM 2).
 RA Brukov K.G., Garcia J.G.N.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
 RN [5]
 RN SEQUENCE OF 923-1914 FROM N.A.
 RC TISSUE=hippocampus;
 RX MEDLINE=96121365; PubMed=8575746;
 RA Potier M.-C., Chelot E., Pekarsky Y., Gardiner K., Rossier J.,
 RA Turnell W.G.;
 RT "The human myosin light chain kinase (MLCK) from hippocampus:
 RT cloning, sequencing, expression, and localization to 3qcen-q21.";
 RL Genomics 29:562-570 (1995).
 RN [6]
 RN SEQUENCE OF 1614-1914 FROM N.A.
 RC TISSUE=Lung, and Placenta;
 RX MEDLINE=20007838; PubMed=10536370;
 RA Watterson M.D., Schavocky J.P., Guo L., Weiss C., Chlenski A.,
 RA Shinsky V.P., Van Eldik L.J., Haiech J.;
 RT "Analysis of the kinase-related protein gene found at human chromosome
 RT 3q21 in a multi-gene cluster: organization, expression, alternative
 RT splicing and polymorphic marker.";
 RL J. Cell. Biochem. 75:481-491 (1999).
 RN [7]
 RN SEQUENCE OF 1456-1914 FROM N.A.
 RC TISSUE=Placenta;
 RX Watterson M.D.;
 RA Submitted (NOV-1995) to the EMBL/GenBank/DBSJ databases.
 CC -!- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
 CC SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
 CC IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC), AN EVENT THAT
 CC FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS. CENTRAL
 CC DETERMINANT IN THE DEVELOPMENT OF VASCULAR PERMEABILITY AND TISSUE
 CC EDENIA FORMATION. IN THE NERVOUS SYSTEM IT HAS BEEN SHOWN TO
 CC CONTROL THE GROWTH INITIATION OF ASTROCYTIC PROCESSES IN CULTURE
 CC AND TO PARTICIPATE IN TRANSMITTER RELEASE AT SYNAPSES FORMED
 CC BETWEEN CULTURED SYMPATHETIC GANGLION CELLS. CRITICAL PARTICIPANT
 CC IN SIGNALING SEQUENCES THAT RESULT IN FIBROBLAST APOPTOSIS.
 CC -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
 CC light-chain] phosphate.
 CC -!- SUBUNIT: ISOFORM TELOKIN BINDS CALMODULIN.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=6;
 CC Comment-Additional isoforms seem to exist;
 CC Name=1; Synonyms=Non-muscle isozyme;
 CC IsoId=Q15746-1; Sequence=Displayed;
 CC Note-The smooth muscle isozyme and telokin are produced by
 CC alternative initiation at Met-923 and Met-1761 of isoform 1;
 CC Name=2;
 CC IsoId=Q15746-2; Sequence=VSP_004791;
 CC Name=3A; IsoId=Q15746-3; Sequence=VSP_004792, VSP_004794;
 CC Name=3B;
 CC IsoId=Q15746-4; Sequence=VSP_004791, VSP_004792, VSP_004794;
 CC Name=4;
 CC IsoId=Q15746-5; Sequence=VSP_004792, VSP_004793;
 CC Name=Del-1790;
 CC IsoId=Q15746-6; Sequence=VSP_004795;
 CC Event-Alternative initiation;
 CC Comment=3 isoforms, 1/Non-muscle isozyme (shown here),
 CC smooth-muscle isozyme and telokin, are produced by alternative
 CC initiation at Met-1, Met-923 and Met-1761. Telokin has no
 CC catalytic activity;
 CC -!- TISSUE SPECIFICITY: SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES ARE
 CC EXPRESSED IN A WIDE VARIETY OF ADULT AND FETAL TISSUES AND IN
 CC CULTURED ENDOTHELIUM WITH QUALITATIVE EXPRESSION APPEARING TO BE
 CC NEITHER TISSUE- NOR DEVELOPMENT-SPECIFIC. NON-MUSCLE ISOFORM 2 IS
 CC THE DOMINANT SPICE VARIANT EXPRESSED IN VARIOUS TISSUES. TELOKIN
 CC HAS BEEN FOUND IN A WIDE VARIETY OF ADULT AND FETAL TISSUES.
 CC -!- PTM: MLCK IS PROBABLY DOWN-REGULATED BY PHOSPHORYLATION.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC -!- SIMILARITY: Contains 9 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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ENBL; A48959; AAC18423.2;	-
ENBL; AF069601; AAD15921.2;	-
ENBL; AF069602; AAD15922.1;	-
ENBL; AF069603; AAD15923.1;	-
ENBL; AF069604; AAD15924.1;	-
ENBL; AS5337; CAAS9685.1;	-
ENBL; AF06771; AADS1380.1;	-
ENBL; AF06766; AADS1380.1;	JOINED.
ENBL; AF096767; AADS1380.1;	JOINED.
ENBL; AF096768; AADS1380.1;	JOINED.
ENBL; AF096769; AADS1380.1;	JOINED.
ENBL; AF096770; AADS1381.1;	JOINED.
HSP; Q63450; IAO6.	
Gnew; HGNC:7590; MYLK.	
MIM; 600922;	-
GO; GO:0004687; F-Myosin-light-chain kinase activity; TAS.	
GO; GO:0005468; P-Protein amino acid phosphorylation; TAS.	
InterPro; IPRO08957; FN_III-like.	
InterPro; IPRO03961; FN_III.	
InterPro; IPRO07110; IG-Like.	
InterPro; IPRO00719; Prot.kinase.	
InterPro; IPRO08271; Ser_thr_pkin_AS.	
Pfam; PF00041; fn3; 1.	
Pfam; PF00047; ig; 8.	
Pfam; PF00069; pkinase; 1.	
ProdDom; PD000001; Prot.kinase; 1.	
PROSITE; PSS0835; IG_LIKE; 9.	
PROSITE; PSS0107; PROTEIN_KINASE_ATP; 1.	
PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.	
PROSITE; PSS0108; PROTEIN_KINASE_ST; 1.	
Transferase; Serine/threonine-protein_kinase; Calmodulin-binding;	
ATP-binding; Phosphorylation; immunoglobulin domain; Repeat;	
Alternative initiation; Alternative splicing.	
CHAIN 1 1914	
MYOSIN LIGHT CHAIN KINASE, ISOFORM NON-MUSCLE ISOZYME.	
CHAIN 923 1914	
SMOOTH-MUSCLE ISOZYME.	
CHAIN 1761 1914	
MYOSIN LIGHT CHAIN KINASE, ISOFORM TELOKIN.	
FOR ISOFORM SMOOTH-MUSCLE ISOZYME.	
INIT_MET 923 923	
INIT_MET 1761 1761	
DOMAIN 33 122	
IG-LIKE C2-TYPE 1.	
DOMAIN 161 249	
IG-LIKE C2-TYPE 2.	
DOMAIN 414 503	
IG-LIKE C2-TYPE 3.	
DOMAIN 514 599	
IG-LIKE C2-TYPE 4.	
DOMAIN 620 711	
IG-LIKE C2-TYPE 5.	
DOMAIN 721 821	
IG-LIKE C2-TYPE 6.	
DOMAIN 1038 1186	
IG-LIKE C2-TYPE 7.	
DOMAIN 1238 1266	
IG-LIKE C2-TYPE 8.	
DOMAIN 1343 1413	
FIBRONECTIN TYPE-III.	
DOMAIN 1464 1719	
PROTEIN_KINASE.	
DOMAIN 1711 1774	
CALMODULIN-BINDING.	
DOMAIN 1809 1898	
IG-LIKE C2-TYPE 9.	
NF BIND 1470 1478	
ATP (BY SIMILARITY).	
BINDING 1493 1493	
ATP (BY SIMILARITY).	
ACT_SITE 1585 1585	
BY SIMILARITY.	
POLY-GLU.	
DOMAIN 1906 1914	
S X 28 AA APPROXIMATE TANDEM REPEATS.	
DOMAIN 868 998	
REPEAT 868 895	
I-1.	
REPEAT 896 923	
I-2.	

[illegible]

RESULT 5	SMILES	CHICK	STANDARD;	PRT;	1906 AA.
1	CC(C)C	1	1	1	1
2	CC(C)C	1	1	1	1
3	CC(C)C	1	1	1	1
4	CC(C)C	1	1	1	1
5	CC(C)C	1	1	1	1
6	CC(C)C	1	1	1	1
7	CC(C)C	1	1	1	1
8	CC(C)C	1	1	1	1
9	CC(C)C	1	1	1	1
10	CC(C)C	1	1	1	1
11	CC(C)C	1	1	1	1
12	CC(C)C	1	1	1	1
13	CC(C)C	1	1	1	1
14	CC(C)C	1	1	1	1
15	CC(C)C	1	1	1	1
16	CC(C)C	1	1	1	1
17	CC(C)C	1	1	1	1
18	CC(C)C	1	1	1	1
19	CC(C)C	1	1	1	1
20	CC(C)C	1	1	1	1
21	CC(C)C	1	1	1	1
22	CC(C)C	1	1	1	1
23	CC(C)C	1	1	1	1
24	CC(C)C	1	1	1	1
25	CC(C)C	1	1	1	1
26	CC(C)C	1	1	1	1
27	CC(C)C	1	1	1	1
28	CC(C)C	1	1	1	1
29	CC(C)C	1	1	1	1
30	CC(C)C	1	1	1	1
31	CC(C)C	1	1	1	1
32	CC(C)C	1	1	1	1
33	CC(C)C	1	1	1	1
34	CC(C)C	1	1	1	1
35	CC(C)C	1	1	1	1
36	CC(C)C	1	1	1	1
37	CC(C)C	1	1	1	1
38	CC(C)C	1	1	1	1
39	CC(C)C	1	1	1	1
40	CC(C)C	1	1	1	1
41	CC(C)C	1	1	1	1
42	CC(C)C	1	1	1	1
43	CC(C)C	1	1	1	1
44	CC(C)C	1	1	1	1
45	CC(C)C	1	1	1	1
46	CC(C)C	1	1	1	1
47	CC(C)C	1	1	1	1
48	CC(C)C	1	1	1	1
49	CC(C)C	1	1	1	1
50	CC(C)C	1	1	1	1
51	CC(C)C	1	1	1	1
52	CC(C)C	1	1	1	1
53	CC(C)C	1	1	1	1
54	CC(C)C	1	1	1	1
55	CC(C)C	1	1	1	1
56	CC(C)C	1	1	1	1
57	CC(C)C	1	1	1	1
58	CC(C)C	1	1	1	1
59	CC(C)C	1	1	1	1
60	CC(C)C	1	1	1	1
61	CC(C)C	1	1	1	1
62	CC(C)C	1	1	1	1
63	CC(C)C	1	1	1	1
64	CC(C)C	1	1	1	1
65	CC(C)C	1	1	1	1
66	CC(C)C	1	1	1	1
67	CC(C)C	1	1	1	1
68	CC(C)C	1	1	1	1
69	CC(C)C	1	1	1	1
70	CC(C)C	1	1	1	1
71	CC(C)C	1	1	1	1
72	CC(C)C	1	1	1	1
73	CC(C)C	1	1	1	1
74	CC(C)C	1	1	1	1
75	CC(C)C	1	1	1	1
76	CC(C)C	1	1	1	1

DE (EC 2.7.1.117) (MLCK) [Contains: Telokin].

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_taxid=9031;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM MLCK-210).

RX MEDLINE=96033976; PubMed=7589469;

RA Waterson D.M., Collinge M., Lukas T.J., van Eldik L.J., Birukov K.G.,

RA Stepanova O.V., Shirinsky V.P.;

RT "Multiple gene products are produced from a novel protein kinase

RT transcription region".

RL FEBS Lett. 373:217-220 (1995).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM MLCK-108).

RX MEDLINE=90192792; PubMed=2315320;

RA Olson N.J., Pearson R.B., Needleman D.S., Hurwitz M.J., Kemp B.E.,

RA Means A.R.;

RT "Regulatory and structural motifs of chicken gizzard myosin light

RT chain kinase".

RL Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288 (1990).

RN [3]

RP SEQUENCE OF 649-1906 FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Fibroblast;

RX MEDLINE=903161738; PubMed=2202734;

RA Shoemaker M.O., Lau W., Shattuck R.L., Kwiatkowski A.P.,

RA Marislian P.E., Guerra-Santos L., Wilson E., Lukas T.J.,

RA van Eldik L.J., Waterson D.M.;

RT "Use of DNA sequence and mutant analyses and antisense

RT oligodeoxynucleotides to examine the molecular basis of nonmuscle

RT myosin light chain kinase autoinhibition, calmodulin recognition, and

RT activity".

RL J. Cell Biol. 111:1107-1125 (1990).

RN [4]

RP SEQUENCE OF 1259-1906 FROM N.A.

RC TISSUE=Gizzard;

RX MEDLINE=87157587; PubMed=3030394;

RA Guerrero V. Jr., Russo M.A., Olson N.J., Putkey J.A., Means A.R.;

RA "Domain organization of chicken gizzard myosin light chain kinase

RA deduced from a cloned cDNA".

RL Biochemistry 25:8372-8381 (1986).

RN [5]

RP SEQUENCE OF 1750-1906 FROM N.A. (ISOFORM TELOKIN).

RC TISSUE=Gizzard;

RX MEDLINE=93073972; PubMed=1444462;

RA Yoshikai S., Ikebe M.;

RT "Molecular cloning of the chicken gizzard telokin gene and cDNA".

RL Arch. Biochem. Biophys. 299:242-247 (1992).

RN [6]

RP SEQUENCE OF 1750-1906 FROM N.A. (ISOFORM TELOKIN).

RX MEDLINE=92236611; PubMed=1373815;

RA Collinge M., Matrisian P.E., Zimmer W.E., Shattuck R.L., Lukas T.J.,

RA van Eldik L.J., Waterson D.M.;

RT "Structure and expression of a calcium-binding protein gene contained

RT within a calmodulin-regulated protein kinase gene".

RL Mol. Cell. Biol. 12:2359-2371 (1992).

CC -!- FUNCTION: Phosphorylates a specific serine in the N-terminus of a

CC myosin light chain, which leads to the formation calmodulin/MLCK

CC signal transduction complexes which allow selective transduction

CC of calcium signals.

CC -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin

CC light-chain] phosphate.

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative initiation;

CC Comment=At least 3 isoforms, MLCK-210/Non-muscle,

CC MLCK-108/Smooth-muscle and Telokin, are produced by alternative

CC initiation;

CC -!- TISSUE SPECIFICITY: ISOFORM TELOKIN IS EXPRESSED IN GIZZARD,

CC HEART, LUNG, INTESTINE, AND SKELETAL MUSCLE ALTHOUGH THE LEVELS OF

CC THE EXPRESSION IN THE LATTER WERE MUCH LESS THAN THAT IN THE

CC GIZZARD.

CC -!- DOMAIN: TELOKIN BINDS CALMODULIN.

CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

CC -!- SIMILARITY: Contains 9 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

CC -----

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X52876; CAA37056.1; -

DR EMBL; X52876; CAA37057.1; -

DR EMBL; X52876; CAA37058.1; -

DR EMBL; M31048; AAA49069.1; -

DR EMBL; M14953; AAA69964.1; -

DR EMBL; M96655; AAA49083.1; -

DR EMBL; M82883; AAA48647.1; -

DR EMBL; M82884; AAB53768.1; -

DR PIR; S68235; S68235.

DR PDB; 1CDL; 31-AUG-94.

DR PDB; 1VRK; 27-APR-99.

DR InterPro; IPR008957; FN_III-like.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR008271; Ser_thr_pkinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR Pfam; PF00041; fn3; 1.

DR Pfam; PF00047; ig; 9.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00060; FN3; 1.

DR SMART; SM00408; IG2; 8.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00835; IG_LIKE; 9.

DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;

KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;

KW Alternative initiation; 3D-structure.

FT CHAIN 1 1906 MYOSIN LIGHT CHAIN KINASE, ISOFORM MLCK-

FT FT 935 1906

FT CHAIN 1750 1906

FT CHAIN 1750 1906

FT INIT_MET 935 935

FT INIT_MET 1750 1750

FT DOMAIN 128 117

FT DOMAIN 156 244

FT DOMAIN 429 517

FT DOMAIN 521 613

FT DOMAIN 637 725

FT DOMAIN 735 830

FT DOMAIN 1084 1172

FT DOMAIN 1225 1313

FT DOMAIN 1330 1400

FT DOMAIN 1453 1708

FT DOMAIN 1794 1885

FT NP_BIND 1459 1467

FT BINDING 1482 1482

FT ACT_SITE 1574 1574

FT DOMAIN 1716 1728

FT DOMAIN 1730 1749

FT DOMAIN 1317 1364

FT DOMAIN 1385 1402

FT DOMAIN 660 1833

FT

FT REPEAT 660 676 IIA-1.
 FT REPEAT 758 774 IIA-2.
 FT REPEAT 1107 1123 IIA-3.
 FT REPEAT 1817 1833 IIA-4.
 FT DOMAIN 693 1866 5 X REPEATS, MOTIF IIB.
 FT REPEAT 693 708 IIB-1.
 FT REPEAT 791 807 IIB-2.
 FT REPEAT 1140 1156 IIB-3.
 FT REPEAT 1281 1297 IIB-4.
 FT REPEAT 1851 1866 IIB-5.
 FT DOMAIN 970 1226 4 X REPEATS, MOTIF III.
 FT REPEAT 970 987 IIB-1.
 FT REPEAT 999 1016 IIB-2.
 FT REPEAT 1061 1078 IIB-3.
 FT REPEAT 1209 1226 IIB-4.
 FT DOMAIN 1700 1763 CALMODULIN-BINDING.
 FT DOMAIN 1896 1906 POLY-GLU.
 FT MOD RES 1748 1748 PHOSPHORYLATION.
 FT MOD RES 1762 1762 PHOSPHORYLATION.
 FT CONFLICT 1439 1439 R->Q (IN REF. 4).
 SQ SEQUENCE 1906 AA; 210445 MW; AD7DBA3B69EE3363 CRC64;

Query Match 6.1%; Score 532; DB 1; Length 1906;
 Best Local Similarity 20.5%; Pred. No. 1.4e-11;
 Matches 397; Conservative 233; Mismatches 700; Indels 608; Gaps 83;

QY 48 PALPG-PPSMQVIEDVCAQTGCTAOFEAIIIEGDDPOPSVTWKDSVOLVDSTRLSQOQEG 106
 DB 21 PSVPAEAPATLPPRNIRVQLGATARFEGKVRGYPEPQITWYRNGHPL-----PEG 71
 QY 107 TTY-----SLVLRHVASKDAGVYTCIAONTGGQVLCRAELVLGGD-----NEPDS 152
 DB 72 DHYVVDHSIRGIFSLVKGVEGDSKGTCEAANDGGVQVTVELTVEGNSLKYSLPSS 131
 QY 153 EKQSHRKLHSLFYEVKEIIRGVFGVGRVQH-----KGNKILC-----AAK 194
 DB 132 AKTPGGRL-----SVPPVHRPSTINGSPPKFATKRNVRVREGQTR 174
 QY 195 F-PLRERTRAQ-AYRERDILAAHPLVTGLLDQFETKTLILILECSSEELDR-LY 251
 DB 175 FSKKITRQPQVTVTKGDI-----HLOQNERFNMFE--KTGIQYLEI-QNVQLADAGIY 226
 QY 252 RKGVTYEA-BVKYVIOQLVEGLHYLHSHG-VLHLDIKPSNLMVHPAREDKICDF----- 305
 DB 227 TCTVNSAGASYSASLTWQGPDKTTHAQPLCMFKPTL-----ATKAENSDFKOAT 281
 QY 306 --GPAQNI--TPAELOFSQVGSPEFVSPHIIQONPVSEASDIWANGVYSLSLTCSSPFA 361
 DB 282 SNGIAKELKSTELM-----VETKDRLSAKKETFTYSREAKDGKQ 322
 QY 362 GESDRATLLNVLSGRVSWSPMAAHLSEDAKDFIKATLQAPQAPRPSAAQCLSHFWFLKS 421
 DB 323 GQOQEANVPLOESR-GTKGPQVLQKTSITILQAVKAQPEKAEPTT-----FIHQ 374
 QY 422 MPABEAHFINTKOLKFLARSWRORSLSYKSIILVMSRIPELLRPPDSPSLGVARHLCR 481
 DB 375 --AED-----RKRTVQPLMTTT-----QENPSL----- 396
 QY 482 DTGSSSSSSSSONELAPPARAKSLPPSVTHSLPHRGLRPSASLPBBAEASE----- 537
 DB 397 -TQVSPRSTENRAGVKSVKEEKREPLGLIPQFESR-----PQLEHSEGOEI 446
 QY 538 -----RSTAPAPAPASPEGAGPPAAQO---CVPRHSVIRSLFVHOA---GESPEHGALAPGS 588
 DB 447 KFKSKVSGKPKDPVFWFKGVPIKTGEGIQIYEEDGTHCLMLKKAACLDGSGSYSCAAFPN 506
 QY 589 RHPARR-----RHLLKG-----GYTAGALPLGRPLMEHR 619
 DB 507 RGQTSISWLLTVKRPKVEEVAFCFSSVLGCVISBQDFVLCYVGV-----PVEIT 560
 QY 620 -VLEESAAREEQATLLAKAPSFETALRLPASG---THLAPGHSHLEHDSPT---PRPS 672
 DB 561 WLLNEQPIQYAHSTFEAGVAKLTVDQALPEDDGIYTCLEANNAGRASCQAQVTVKEKSS 620

QY 673 SEACG-EAORLP8--APSGAIPRDMGHPOGSKQIPLSTGGHPTAQPERPSPD8PW----- 725
 DB 621 KKAEGTQAAKANKTAPIFLKLGLTDLKVMGDSQVINT-----VEVSANPCPEIITWLNHG 674
 QY 726 ---GQAPAPCHPKQ3SA---PQEGCSHPAPVAPCPGSPFPSPGCK-----EAPL 768
 DB 675 KEIQETEDFHFEKKGNEYSLYIQE-----VFPEDTGKY--TCEAMNELGETQTOATL 724
 QY 769 VPSP-----FLGQOPAPPAPAKASPLDSKMGPGDISLPGRP-----KGPCCSP 814
 DB 725 TVQEPQDGIQPMFISKPRSVTAAGQNVLI-----SCAIGADFFPTVHVFKQGEITP 777
 QY 815 GSASQASSSQ-----VSSLRVGS-----SQVTEPGPSLD---AEGMTQEAEDLS 856
 DB 778 GTGCEILQNEIDFTLIRNVQSRHAGQYELQIRNVQV-ECSCQVSLMLRESSASRAEMLR 836
 QY 857 DSPPTLQRPQEQVTRKESLGR--GGVAGVAGYGTFAFGDAGGMLQGQPMWARIANAV 914
 DB 837 DGRESA-----SSGERRDGG--NYGALTFGRTSG-----FKK 866
 QY 915 S0SE-----EEQEEARAESQSEEQEARARAGPLQVPSARPPVPEVGRAPTRSPPEPTWED 970
 DB 867 S8SETRAAEEQEDVRGLKRRVETREHTESLRQEAQ----- 906
 QY 971 IGOVSIQVIRDLSDGAADTISLDISEVDPAYLNSLDYIKYLPREFMIFRKYVPSAQ 1030
 DB 907 -----LDFRDLGKKVTKSFSEB-----DKETPAEQMDFR--ANLQR 943
 QY 1031 PBPSPMAEE-----LAEFPPTWMPGELGPHAGLEITESESDVDALLA 1076
 DB 944 QVKPTLSSEERKCHAPQOVDFRSVLAKKGTPTLPKPKVPPKP-AVTD-----F 993
 QY 1077 EAAVGRKR-----WSPP-----SRSLFHPFGRHLPLDEPAELGLRERVKASVEHI 1122
 DB 994 RSVLGAKKPPAENGASATPAPNABAGSEAQNATPENSEAPAKPV-VKKEEKNDKCEHG 1052
 QY 1123 SRILKRPGLKEGPPKPKGLASRLSGLSKWDRAPTFLRELSDETIVLQSVTLACQ 1182
 DB 1053 CAWVDGGIIGKKAENK-----AASKETPPSKGTAPSTFKLODAKADGKLVQCR 1106
 QY 1183 VSAQPAQAQWKSQCAPLESRRVLIS--ATLKNFQLLTILVVAEDLVGVTVCSVSNALG 1240
 DB 1107 ISSDPASVSWTLDKSKAKSSKSIVISQEGTLC--LTIEKWPEGEGEYKCIENAAAG 1163
 QY 1241 -----TVTTTGVLRKAER-----PSSSP 1258
 DB 1164 KACACKVLVEDTSTKAAPKPKTKPTLPPVLSTESSEATVKKKPAKTPPKAAT 1223
 QY 1259 CPDICEVYADGVLVWKPVSYSYGPV----- 1283
 DB 1224 PPOITQFPEDRKVRAGESVELFAKVGTAPITCTTWKFKQIQENYIKIENAESSKLT 1283
 QY 1284 -----TYIVQ-----CS 1290
 DB 1284 ISSTKQEHCGCYTLVVENKLGSRQAQVNLTVYDKPDPAGTPPCASDIRSSSLTSLWSYGS 1343
 QY 1291 LEGGS-----WTLASDIFDCCYLT--KLSRGGTITFTTACVSKAG 1330
 DB 1344 YDGGSAVQSYTVIWNVSVDNKNKTDLT-----CRSTSFNVQDLQADREYKFRVRAANVYG 1398
 QY 1331 MGPIYSPSEVLLG--GPSHLASEE---ESQGRSAQPLSTKT-----FAFOTQ 1374
 DB 1399 ISEPSQSEVWVKVQBKEELKEEELSDDEGKETEVNRYTIVTINTEKQVSDVYNTIEER 1458
 QY 1375 ICRGRFSVVRQCEWKASGALAAKII-PYHPKDKTAVLRVEYALKGLRHPHPLAOLHAAYL 1433
 DB 1459 LOSGKFGQVRLVEKTKWAGKFFKAYSAXEKENIRDEISINWCLHHPKLQCVDAFE 1518
 QY 1434 SPRHLVILIELCSGPELLP-CLAFRASYSSEVKDYLMQMLSATQYLNQHILHLDLRSE 1492
 DB 1519 EKANTVMVLEWVGSGELFERIIDEDELFETERECIKYMRQISEGVEYTHKQIVHLDLRKE 1578

QY 1493 NMITEY--NLLKVVLDGNAQSLSQE---KVLPSDKFKDYLETMADELLEGOGAVPQTDI 1547
 DB 1579 NIMCVNTGTSIKLIDFGLARRIESAGSLKVLFGTP-----EFVAPEVINYPLOYETDM 1633
 QY 1548 WAIGTAFIMLSBEPVSSSECCARDLQGLKGLVRL-SRCYAGLSGCAVAFRLSRSTLCAQP 1606
 DB 1634 WSGIVCIVLVSGLSPMGNDNETLANVTSATWDFDEAFDEISDDAKDFISNLLKXDM 1693
 QY 1607 WGREPCASSCLOCPKLTSE 1624
 DB 1694 KSLRNCTQCLQHPWLQKD 1711

RESULT 6
 ID_DAK3_MOUSE STANDARD; PRT; 448 AA.
 AC 054784;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Death-associated protein kinase 3 (EC 2.7.1.37) (DAP kinase 3) (DAP-
 DE like kinase) (Dlk) (ZIP-kinase).
 GN DAPK3 OR ZIPK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, INTERACTION WITH
 RP ATP4, SUBCELLULAR LOCATION, AND MUTAGENESIS OF LYS-42; VAL-422;
 RP VAL-429 AND LEU-436.
 RX MEDLINE=98147805; PubMed=9488481;
 RA Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;
 RT "ZIP-kinase, a novel serine/threonine kinase which mediates
 RT apoptosis";
 RL Mol. Cell. Biol. 18:1642-1651(1998).
 RN [2]

SUBCELLULAR LOCATION, AND INTERACTION WITH DAXX AND PAWR.
 RP MEDLINE=22799111; PubMed=12917339;
 RA Kawai T., Akira S., Reed J.C.;
 RT "ZIP kinase triggers apoptosis from nuclear PML oncogenic domains.";
 RL Mol. Cell. Biol. 23:6174-6186(2003).
 CC -!- FUNCTION: Serine/threonine kinase which acts as a positive
 CC regulator of apoptosis.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- COFACTOR: Magnesium.
 CC -!- SUBUNIT: Homodimer or forms heterodimers with ATF4. Both
 CC interactions require an intact leucine zipper domain and
 CC oligomerization is required for full enzymatic activity. Also
 CC binds to DAXX and PAWR, possibly in a ternary complex which plays
 CC a role in caspase activation.
 CC -!- SUBCELLULAR LOCATION: Nuclear. Relocates to the cytoplasm on
 CC binding PAWR where the complex appears to interact with actin
 CC filaments.
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, lung,
 CC skeletal muscle, kidney and testis. Lower levels in liver and
 CC spleen.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. DAP
 CC kinase subfamily.

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 entities requires a license agreement (See <http://www.ebi.ac.uk/ebis/sequence/10090>)
 or send an email to license@ebi.ac.uk.

 DB EMBL; AB007143; BAA24954.1; -
 DB HSSP; O63450; 1A06.
 DB MGD; MG1:1203520; DapK3.
 DB InterPro; IPR000719; Prot_kinase.
 DB InterPro; IPR002290; Ser_Ehr_Pkinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00101; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Apoptosis;
 KW Nuclear protein.
 FT DOMAIN 13 275 PROTEIN KINASE.
 FT NP_BIND 19 27 ATP (BY SIMILARITY).
 FT BINDING 42 42 ATP.
 FT ACT_SITE 139 139 BY SIMILARITY.
 FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
 FT MUTAGEN 422 422 V->A: DECREASED ACTIVITY; WHEN ASSOCIATED
 FT WITH A-429 AND A-436.
 FT MUTAGEN 429 429 V->A: DECREASED ACTIVITY; WHEN ASSOCIATED
 FT WITH A-422 AND A-436.
 FT MUTAGEN 436 436 L->A: DECREASED ACTIVITY; WHEN ASSOCIATED
 FT WITH A-422 AND A-429.
 SQ SEQUENCE 448 AA; 51421 MW; DA32EF3EB1F20EFC CRC64;
 Query Match 5.6%; Score 489; DB 1; Length 448;
 Best Local Similarity 38.1%; Pred. No. 1,1e-10;
 Matches 114; Conservative 56; Mismatches 117; Indels 12; Gaps 5;
 QY 165 YEVKEIGRGVGFVKRVQHKNGKILCAAKFTPLR-----SR---TRAQAYRERDILALS 217
 DB 13 YEMGEELGSGQPAIVKRCQCKGTGMEYAAKFIKGRLPSSRGVSREREIERSVILREIR 72
 QY 218 HPVVTGLDQFETRTKLILILELCSSEELDLRYKGVVTVAEVKVYIQQLVEGLHYLHS 277
 DB 73 HPNIITLHDVFENKTDVLLILELVSGGELFDLAEKESLDEDEATQFLKQLDGVHYLHS 132
 QY 278 HGVHLJDIKPSNLMV--HPAREDIKICDFGPAQNTPAELQFSQYSGSPFVSPILIQON 335
 DB 133 KRIAHDLPENIMLLDKEAASPRIKLIDFGIAHREAGSEFKNIFGTGTFVAPVINYE 192
 QY 336 PVSEASDIWAMGVISYLSLTSCSPAGESDRATLNLVLEGRVSWSSPMAAHLSEDAKDFI 395
 DB 193 PLGLEADMSIGVITVILLSGASPFIGETKQETLNLISAVNYDFDEYFSSSELAKDFI 252
 QY 396 KATLQAPQAPSAACQLSHPWFLKSPABEAHFINTKQLKELLARSWQRLMSYKSI 454
 DB 253 RLLLVKDPKRRMTIAQSLSHSWMKVRREDGARKPERRLR--AARLR-EYSLKSHSM 308

RESULT 7
 ID_DAK3_RAT STANDARD; PRT; 448 AA.
 AC 088764;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Death-associated protein kinase 3 (EC 2.7.1.37) (DAP kinase 3) (DAP-
 DE like kinase) (Dlk) (ZIP-kinase).
 GN DAPK3 OR ZIPK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND SUBCELLULAR
 RP LOCATION.
 RX MEDLINE=99054663; PubMed=9840928;
 RA Kogel D., Pictner O., Landsberg G., Christian S., Scheidtmann K.H.;
 RT "Cloning and characterisation of Dlk, a novel serine/threonine kinase
 RT that is tightly associated with chromatin and phosphorylates core
 RT histones.";
 RL Oncogene 20:2645-2654(1998).
 RN [2]
 RP FUNCTION: INTERACTION WITH ATF4 AND PAWR, SUBCELLULAR LOCATION, AND
 RP MUTAGENESIS OF LYS-42.


```

RX MEDLINE=20071105; PubMed=10602480;
RT Page G., Kogel D., Rangnekar V., Scheidtmann K.H.;
RL "Interaction partners of Plk2/ZIP kinase: co-expression of Plk2/ZIP
RL kinase and Par-4 results in cytoplasmic retention and apoptosis.";
RL Oncogene 18:7265-7273(1999).
CC -!- FUNCTION: Serine/threonine kinase which acts as a positive
CC regulator of apoptosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a
CC phosphateprotein.
CC -!- COFACTOR: Magnesium.
CC -!- SUBUNIT: Homodimer or forms heterodimers with ATF4. Both
CC interactions require an intact leucine zipper domain and
CC oligomerization is required for full enzymatic activity. Also
CC binds to DAXX and PAMR, possibly in a ternary complex which plays
CC a role in caspase activation.
CC -!- SUBCELLULAR LOCATION: Nuclear. Relocates to the cytoplasm on
CC binding PAMR where the complex appears to interact with actin
CC filaments.
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed in all tissue types
CC examined. High levels in brain, heart, lung and spleen, lower
CC expression in kidney, liver, skeletal muscle and testis.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. DAP
CC kinase subfamily.
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
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DR EMBL; AJ006971; CAA07360.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00069; pKinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Apoptosis;
KW Nuclear protein.
KW DOMAIN 13 275 PROTEIN KINASE.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP.
FT ACT_SITE 139 139 BY SIMILARITY.
FT MUTAGEN 42 42 K-EA: LOSS OF KINASE ACTIVITY AND OF
FT TRANSLOCATION INTO THE CYTOPLASM.
FT FT FT MISSING: PREVENTS BINDING TO ATF4 BUT NOT
FT WT.
SQ SEQUENCE 448 AA; 51449 MW; 843C0FB0FCBCEA CRC64;
Query Match 5.6%; Score 489; DB 1; Length 448;
Best Local Similarity 38.1%; Pred. No. 1.1e-10;
Matches 114; Conservative 56; Mismatches 117; Indels 12; Gaps 5;
QY 165 YEVEKEETGRGVGPKVQKHGNKILCAAKFFTLR-----SR---TRACAYVERDILAALS 217
DB 13 YEMGEELSGOFALVRCKQQGTGMVAKFKIKRLPSRRGVSREIEREIVSLIREIR 72
QY 218 HPLVTGLLDQFSTRKTLLILELCSEELLDRLYRGVVTEAEVKYIQQLVEGLHYLHS 277
DB 73 HFNIITLHDVFENKTDVVLLELVSGSELFDFLAEKESLTEDEAQTFKLQDLGGVHYLHS 132
QY 278 HGVLHLDKPSNLNW--HPAREDIKIDCFGAQNITPAELQFSYGSPFPVSPFIQQN 335
DB 133 KEIAHFCLKPENIMLDKHAASPRIKLDFGTAHRIEAGSEPFKNIFGFPEFAEIYNVE 192
QY 336 PVRSASDIWANGVISYLUSLTCSPSFAGESSDRATLLNVLEGTVSWSSPNWAHLSEDADKFI 395

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193 PIGLEADMWSIGVITYILLGASFFLGKQETLTNISAVNYDFEYFSGTSELAKDFTI 253

396 XATLQAPQAPRPSAAQCILSHFWFLKSPABEAHPINTKQLFLIARSRWQSRMSYKSI 454

253 RLLLVKDKPRRTWITIAQSLSHSNIKVRRREDGAKPERRLR--AARLR-BYSLKSHSSM 308

RESULT 8

DAK2_MOUSE

ID DAK2_MOUSE STANDARD; PRT; 370 AA.

AC Q8VDF3; O88861; Q9QYM4;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Death-associated protein kinase 2 (EC 2.7.1.37) (DAP kinase 2) (DAP-

DE kinase related protein 1) (DRP-1).

GN DAPK2.

CS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RP [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=99303018; PubMed=10376525;

RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,

RA Jenkins T., Akira S.;

RT "Death-associated protein kinase 2 is a new calcium/calmodulin-

RT dependent protein kinase that signals apoptosis through its catalytic

RT activity.";

RL Oncogene 18:3471-3480(1999).

RN [2]

RN SEQUENCE FROM N.A.

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,

RA Tapaltero M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein L.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Hellon E., Kettman M., Madan A.C., Shevchenko Y., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalski M., Smalley D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences".

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RN SEQUENCE OF 68-370 FROM N.A.

RX MEDLINE=20094983; PubMed=10629061;

RA Inbal B., Shani G., Cohen O., Kissil J.L., Kimchi A.;

RT "Death-associated protein kinase-related protein 1, a novel

RT serine/threonine kinase involved in apoptosis.";

RL Mol. Cell. Biol. 20:1044-1054(2000).

CC -1- FUNCTION: Calcium/calmodulin-dependent serine/threonine kinase

CC which acts as a positive regulator of apoptosis (By

CC similarity).

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -1- COFACTOR: Magnesium (By similarity).

CC -1- ENZYME REGULATION: Negatively regulated by autophosphorylation on

CC Ser-308 (By similarity).

CC -1- SUBUNIT: Homodimer. Homodimerization is required for apoptotic

CC function and is inhibited by autophosphorylation at Ser-308 (By

CC similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the Ser/thr family of protein kinases. DAP

CC kinase subfamily.

P53355; Q9BTL8;
01-OCT-1996 (Rel. 34, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Death-associated protein kinase 1 (EC 2.7.1.37) (DAP kinase 1).
DAPK1 OR DAPK.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1] _SEQUENCE FROM N.A., FUNCTION, INDUCTION, AND MUTAGENESIS OF LYS-42.
MEDLINE=95129831; PubMed=7828849;
Dedes L.P., Feinstein E., Barisgi H., Cohen O., Kimchi A.;
"Identification of a novel serine/threonine kinase and a novel 15-kD
protein as potential mediators of the gamma interferon-induced cell
death.";
Genes Dev. 9:15-30 (1995).
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GAasterland T., Gariboldi M., Gisel C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
 RA Maglott D.R., Maltchin L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wainwright C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Landier E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RT Nature 420:563-573 (2002).
 RL -!- FUNCTION: Calcium/calmodulin-dependent serine/threonine kinase.
 CC Isoform 1 is a negative regulator of apoptosis in direct contrast
 CC to its human homolog. Isoform 2 has no effect on apoptosis and its
 CC function is unknown.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- COFACTOR: Magnesium.
 CC -!- ENZYME REGULATION: Negatively regulated by autophosphorylation on
 CC Ser-308 (by similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonym=Beta;
 CC IsoId=Q80Y7-1; Sequence=Displayed;
 CC Name=2; Synonym=Alpha;
 CC IsoId=Q80Y7-2; Sequence=VSP_050629;
 CC -!- TISSUE SPECIFICITY: High levels in bladder, uterus, vas deferens,
 CC lung, liver and kidney.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. DAP
 CC kinase subfamily.
 CC -!- SIMILARITY: Contains 10 ANK repeats.
 CC -!- SIMILARITY: Contains 1 death domain.

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 or send an email to license@isb-sib.ch).

EMBL; AY245540; AA091934.2; -;
 DR EMBL; AY245541; AA091935.1; -;
 DR EMBL; X97048; CA65762.1; -;
 DR EMBL; BC021490; AAH21490.1; ALT_INIT.
 DR EMBL; BC026671; AAH26671.1; -;
 DR EMBL; BC057317; AAH57317.1; -;
 DR EMBL; BC060161; AAH60161.1; -;
 DR EMBL; AK031553; BAB28681.1; -;
 DR MGD; MGI:1916885; Dapki.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002230; Ser_thr_kinase.
 DR Pfam; PF00023; ank; 8.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00248; ANK; 8.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00220; S_TK; 1.

DR PROSITE; PSS0088; ANK_REPEAT; 7.
 DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PSS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PSS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis;
 KW Alternative splicing.
 FT DOMAIN 13 275 PROTEIN_KINASE.
 FT DOMAIN 267 334 CALMODULIN-BINDING (BY SIMILARITY).
 FT REPEAT 378 407 ANK 1.
 FT REPEAT 411 440 ANK 2.
 FT REPEAT 444 473 ANK 3.
 FT REPEAT 477 506 ANK 4.
 FT REPEAT 510 539 ANK 5.
 FT REPEAT 543 572 ANK 6.
 FT REPEAT 576 605 ANK 7.
 FT REPEAT 609 638 ANK 8.
 FT REPEAT 875 904 ANK 9.
 FT REPEAT 1164 1196 ANK 10.
 FT DOMAIN 1312 1396 DEATH.
 FT NP_BIND 19 27 ATP (BY SIMILARITY).
 FT BINDING 42 42 ATP (BY SIMILARITY).
 FT ACT_SITE 139 139 BY SIMILARITY.
 FT MOD_RES 308 308 PHOSPHORYLATION (AUTO-) (BY
 FT SIMILARITY).
 FT VARSPIC 1431 1442 Missing (in isoform 2).
 FT CONFLICT 354 354 /FTID=VSP_050629.
 FT CONFLICT 441 441 D -> N (IN REF. 2).
 FT CONFLICT 461 461 K -> Q (IN REF. 3).
 FT CONFLICT 960 960 AAH57317/AAH60161.
 FT CONFLICT 1000 1000 V -> A (IN REF. 2).
 FT CONFLICT 1038 1042 S -> P (IN REF. 2).
 FT CONFLICT 1103 1102 N -> T (IN REF. 2).
 FT CONFLICT 1105 1105 RWLCT -> PMALH (IN REF. 2).
 FT CONFLICT 1442 1442 A -> V (IN REF. 1).
 SQ SEQUENCE 1442 AA; 161440 MW; 243A14D7C6598F63 CRC64;
 Query Match 5.4%; Score 469; DB 1; Length 1442;
 Best Local Similarity 33.5%; Pred. No. 1.6e-09;
 Matches 110; Conservative 64; Mismatches 128; Indels 26; Gaps 5;
 QY 158 RKLLHSEYVEKEIGEGVGFVKRVQHKNTLCAKSTPLR----SR---TRAQAYRER 210
 DB 6 QENVDDYDTGELGSGQFAVVKCKRKSTGLQYAAKFKKRTKSSRRGVSRDIEREV 65
 QY 211 DILAALSHPLVTGLDQFETKTLILILELCSSEELDLRYKGVVTEAEVYVYQQLVE 270
 DB 66 SILKEIRHNPVITLHEVVENKTDVILLELVAGGELPDLAEKESLTEEEATEFLKQILS 125
 QY 271 GLYHLHSHGVHLHDIKPSNLMV--HPAREDIKICDRCGFAQNIPTAEQPSQSGSPPEVS 328
 DB 126 GVYLLSLQIAHFDLKPNIMLLDRNVKPKRIKIDFGLAHKIDFGNEFKNIFGTPEFVA 185
 QY 329 PEIQONPVSEASDIWAMGVISYLSLTCSPPFAGESDRATLLNVLGRVSWSSPMAAHL 388
 DB 186 PEIVNYEPLGLEADNWSIGVITILLGASPLFGDTKQETLANVSAVNYDPEEFFFFNTS 245
 QY 389 EDAKDFIKATLQAPQAPSAQCSHPWF---LKSMPAEAEHFINTKQLKFLALSRW 444
 DB 246 TLAKDFIRLLVDPKRWTKMTQDSLQHPWIKPKTKQALSKASAVNMEKFKFAARKKW 305
 QY 445 Q-----RSLMSYKSIILNRS 459
 DB 306 KQSVRLISLCQLSRSLSRNMSVARS 333
 RESULT 11
 ID_KML2_HUMAN STANDARD; PRT; 595 AA.
 AC Q9H1R3; Q95I84;
 DT 28-FEB-2003 (Rel. 41, Created)

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnierch A., Schein J.G., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 95:16899-16903(2002).
CC -I- FUNCTION: Implicated in the level of global muscle contraction and
cardiac function. Phosphorylates a specific serine in the N-terminus of a myosin light chain.
CC -I- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin light-chain] phosphate.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic. Colocalizes with phosphorylated myosin light chain (RLCP) at filaments of the myofibrils.
CC -I- TISSUE SPECIFICITY: Heart and skeletal muscles. Increased expression in the apical tissue compared to the interventricular septal tissue.
CC -I- DISEASE: Defects in MYLK2 are one of the causes of familial hypertrophic cardiomyopathy (CMH) [MIM:192600]; also known as asymmetric septal hypertrophy (ASH), an autosomal dominant disorder.
CC -I- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
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EMBL; AF325549; AAK15494.1; -;
EMBL; AJ272502; CACB1354.1; -;
EMBL; AL160175; CACL0006.1; -;
EMBL; BC007753; AAH07253.1; -;
Genbank; HGNC:16243; MYLK2.
MIM; 606566; -;
MIM; 192600; -;
HSSP; P00518; IPHK.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_Thr_pkin_AS.
InterPro; IPR002290; Ser_Thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
SMART; SM00219; TyPKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding; ATP-binding; Phosphorylation; Acetylation; Disease mutation.

INIT_MET 0 0 BY SIMILARITY
FT MOD_RES 0 1 ACETYLATION (BY SIMILARITY).
FT DOMAIN 284 539 PROTEIN KINASE.
FT DOMAIN 573 585 CALMODULIN-BINDING (BY SIMILARITY).
FT DOMAIN 260 267 POLY-PRO.
FT PT BIND 290 298 ATP (BY SIMILARITY).
FT BINDING 313 313 ATP (BY SIMILARITY).
FT ACT_SITE 405 405 BY SIMILARITY.
FT VARIANT 86 86 A->V (in CMH); /FTId=VAR_014197.
FT VARIANT 94 94 A->E (in CMH).
FT FTId=VAR_014198.
FT CONFLICT 354 360 IVLEMEY -> GGVCVAHS (IN REF. 4).
SQ SEQUENCE 595 AA; 64553 MW; B52749340A950206 CRC64;

Query Match 5.4%; Score 468.5; DB 1; Length 595;
Best Local Similarity 28.9%; Pred No 7.1e-10;
Matches 129; Conservative 91; Mismatches 171; Indels 55; Gaps 13;
QY 43 LHSSLPALPGPPSNQVTIEDVQQTGTAQFAELIEG-----DPQSVTWYKDVSQVL 94

Db 146 LHS-----PSCFAIISSEKILAKKPPSEASELTFEGVPMTHSTDPRAKAEKGN-L 199
Qy 95 VDSTR-----LSQQEGTYSIVLRHVASKDAGVVTCLAQNTGGQVLC-----KA 139
Db 200 AESQKEVCEKTPGQAGAKMGDTSRGLEFOAVFSEKSEV-----GQALCLTAREE 250
Qy 140 ELLVLGGNEDSPSEKSHR-----KLHSFYEV--KEEIGRGVGFVKRVCHKGNKILC 191
Db 251 DCFQILDCCPPPPAPPPFPRMVELRTGNVSSEFSMNSKEALGGGFGAVCTCMKATGLKL 310
Qy 192 AAKRPIPLRS--TRAQAYRERDILAAALSHPLVTGLLDQDPETKRLILILELCSSEELDLRL 250
Db 311 AAKVJKGTPOKEMVLEIEVMQNLNRNLIQLYAAIETHEIVLFWIEGGELEPERI 370
Qy 251 YRKGV-VTEAEVKVYIQQLVHSHGVHLHDIKPSNLMVHPAREDIKICDFGFAQ 309
Db 371 VDEDVHLTEVDTWVFRQICDGLFMKQVRVHLDLKPELNLICVNTTGHVKKIIDFGLAR 430
Qy 310 NITRAELFOFSQGSSEFVSPELIQONPVSEASDIWAMGVISYLSITCSSPPAGESDRATL 369
Db 431 RYNPEKLVNFGTPEFVSPEVNVVDQISDKTDMMSMGVITMLLSGLSPFLGDDDTETL 490
Qy 370 LNVLEGRVSWSPMAHLSEDAKDPKATLQAPQAPSAQCLSHWFLKSMPEAEAHF 429
Db 491 NNVLSGNVYFDEETFEAYSDEAKDFVSNLIVKQQRARNAAQCLAHWP--LNNL-AEKAKR 548
Qy 430 INTK-----QLKFLARSRWQSLMS 450
Db 549 CNRLKSQILKKYLMKRWKGNFIA 574

RESULT 12

DAK3_HUMAN
ID DAK3_HUMAN STANDARD; PRT; 454 AA.
AC O43293;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Death-associated protein kinase 3 (EC 2.7.1.37) (DAP kinase 3) (DAP-
DE like kinase) (DLK) (ZIP-Kinase).
GN DAPK3 OR ZIPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98147805; PubMed=9488481;
RA Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;
RT "ZIP kinase, a novel serine/threonine kinase which mediates
RT apoptosis".
RL Mol. Cell. Biol. 18:1642-1651(1998).
RN [2]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=99283879; PubMed=10356987;
RA Murata-Hori M., Suizu F., Iwasaki T., Kikuchi A., Hosoya H.;
RT "ZIP kinase identified as a novel myosin regulatory light chain kinase
RT in HeLa cells".
RL FEBS Lett. 451:81-84(1999).
RN [3]
RP FUNCTION, AND INTERACTION WITH DAXX AND PAWR.
RX MEDLINE=2279111; PubMed=12917339;
RA Kawai T., Akira S., Reed J.C.;
RT "ZIP kinase triggers apoptosis from nuclear PML oncogenic domains".;
RL Mol. Cell. Biol. 23:6174-6186(2003).
CC -/- FUNCTION: Serine/threonine kinase which acts as a positive
CC regulator of apoptosis.
CC -/- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -/- COFACTOR: Magnesium.
CC -/- SUBUNIT: Homodimer or forms heterodimers with ATF4. Both
CC interactions require an intact leucine zipper domain and
CC oligomerization is required for full enzymatic activity. Also

CC binds to DAXX and PAWR, possibly in a ternary complex which plays
CC a role in caspase activation.
CC -/- SUBCELLULAR LOCATION: Nuclear. Relocates to the cytoplasm on
CC binding PAWR where the complex appears to interact with actin
CC filaments (By similarity).
CC -/- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. DAP
CC kinase subfamily.
CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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CC

CC ENBL; AB007144; BAA24955.1; -;
CC ENBL; AB022341; BAA81746.1; -;
CC HSP; G63450; 1A06.
CC Genew; HGNC:2676; DAPK3.
CC MIM; 603289; -;
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0004574; F:protein serine/threonine kinase activity; TAS.
CC GO; GO:0006917; P:induction of apoptosis; TAS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002290; Ser Thr kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SMO0220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding; Apoptosis;
KW Nuclear protein.
FT DOMAIN 13 275 PROTEIN KINASE.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
SQ SEQUENCE 454 AA; 52535 MW; 5677308A6A1CF0 CRC64;

Query Match 5.3%; Score 466.5; DB 1; Length 454;
Best Local Similarity 38.9%; Pred. No. 6.4e-10;
Matches 102; Conservative 52; Mismatches 99; Indels 9; Gaps 3;

Qy 165 YEVEEIGRGVGFVKRVQKHGKILCAKFIPLR-----SR---TRAQAYRERDILAAALS 217
Db 13 YEMGEELGSGQFALVRKCRQKGTGKQKAYAKFIKKRLSSRRGVSREIEREYNILREIR 72
Qy 218 HPLVTGLLDQFETKTLILILELCSSEELDLRYKGVVTEAEVKVYIQQLVEGLHYLHS 277
Db 73 HPNITLHDFENKTDVVLILELVSGGELDFLAEKESLHEDATQFLKILDGVHYLHS 132
Qy 278 HGVHLHDIKPSNLMV--HPAREDIKICDFGFAQNTIPFAELQFSQGSPEFVSPEIQQN 335
Db 133 KRIAHFDLKPEINMLLQKNVNPRIKLIDFGIAHKIEAGNEFKNIFGTPEFVAPEIYNYE 192
Qy 336 PVSEASDIWAMGVISYLSITCSSPPAGESDRATLNVLEGRVSWSPMAHLSEDAKDFI 395
Db 193 PLGLEADWMSIGVITYILLGASPFGLGTQKQETLTNISAVNYDFEYFNTSLAKDFI 252
Qy 396 KATLQAPQAPSAQCLSHWP 417
Db 253 RRLIVKDPKRWMTIAQSLEHSM 274

RESULT 13

DAK2_HUMAN
ID DAK2_HUMAN STANDARD; PRT; 370 AA.
AC Q9UIK4; O75892;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)

QW	Transferase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Apoptosis.
QW	DOMAIN 23 285
QW	DOMAIN 277 344
FT	NP BIND 29 37
FT	BINDING 52 52
FT	ACT_SITE 149 149
FT	MCD_RES 318 318
FT	MUTAGEN 52 52
FT	MUTAGEN 299 299
FT	MUTAGEN 299 330
FT	MUTAGEN 318 318
FT	MUTAGEN 318 318
FT	MUTAGEN 320 320
FT	MUTAGEN 323 323
FT	MUTAGEN 329 329
FT	CONFLICT 241 241
FT	CONFLICT 253 253
FT	SEQUENCE 370 AA; 42898 MW; 035E914BBCD881A2 CRC64;
QY	Query Match 5.38; Score 465.5; DB 1; Length 370;
QY	Best Local Similarity 32.4%; Fred. No. 5.7e-10; Gaps 12
QY	Matches 121; Conservative 72; Mismatches 133; Indels 47; Gaps 12
QY	158 RRLSHSYEYKKEIGRGVGFVRRVQHGKNGKILCAAKFIPLR-----SR---TRAQAYRER 210
QY	16 QQKVEDFYDIGELGSGQFAIVKKCREKSTGLEYYAAKFIKKQSRASRRGVSRREIEREV 75
QY	211 DILAALSHPLVTGLDQFETKRLIIILIELCSSELLDELYKGVVTEAEVKVYIQQOLVE 270
QY	76 SILKQVILHNVTIHDVYENRTDVILIELVSGELDFDLAOKESLEEATSFNIKILD 135
QY	271 GLHYLHSHGVHLHLDIKFNSLMV-----HPAREDIKICDFGFAQNTPAELQFSQ-YG 322
QY	136 GVNLYHTKTAHPDLKPFENIMLLDKNIPH-----IKLIDFGLAHEIEDG-VSEPKNIFG 189
QY	323 SPFEVSPETIQQPVSEASDIWAGVSYLSLTCSPPAGESDRATLNLVLEGRVSWSSP 382
QY	190 TPEVAFETIYNYEPLGLEADWISGIVITILLSGASPFUGDTKQETLANITAVSVDFFEE 249
QY	383 MAALHSDAKDFIKATLQAPQAPSAACLSHPWFL-----KSPAPAEAHFINTKOLKF 437
QY	250 FFSQTSLEAKDFIKLLVETKRLTIQELAHAPWITPVDNQQAMVRRES-VVNLLENPRK 308
QY	438 LLASRRQWSLMSYKSL--VMFSIPELLRGPPDSPSLGVARHLCRDTCGGSSSSSSSDN 495
QY	309 QYVRRRWKLS-FVIVLCNHLIRSLMKKVLHLPD-----EDLNCESDT 351
QY	496 ELAPFAKSLPP 508
QY	352 E-EDIARRKALHP 363
QY	RESULT 14
QY	KML2_RABIT
QY	ID KML2_RABIT
QY	AC F07313;
QY	01-APR-1988 (Rel. 07, Created)
QY	01-APR-1990 (Rel. 14, Last sequence update)
QY	28-FEB-2003 (Rel. 41, Last annotation update)

DE Myosin light chain kinase 2, skeletal/cardiac muscle (EC 2.7.1.117)
 DE (MLCK2).
 GN MYLK2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90110242; PubMed=1688558;
 RA Herring B.P., Stull J.T., Gallagher P.J.;
 RT "Domain characterization of rabbit skeletal muscle myosin light chain
 kinase."; J. Biol. Chem. 265:1724-1730(1990).
 RL [2]
 RN SEQUENCE OF 1-603.
 RP MEDLINE=87101105; PubMed=3542042;
 RA Takio K., Blumenthal D.K., Walsh K.A., Titani K., Krebs E.G.;
 RT "Amino acid sequence of rabbit skeletal muscle myosin light chain
 kinase."; Biochemistry 25:8049-8057(1986).
 RL [3]
 RN SEQUENCE OF 295-603.
 RP MEDLINE=86104095; PubMed=3841288;
 RA Takio K., Blumenthal D.K., Edelman A.M., Walsh K.A., Krebs E.G.,
 RA Titani K.;
 RT "Amino acid sequence of an active fragment of rabbit skeletal muscle
 myosin light chain kinase."; Biochemistry 24:6028-6037(1985).
 RL [4]
 RN SUBCELLULAR LOCATION.
 RP MEDLINE=21590235; PubMed=11733062;
 RA Davis J.S., Hassanadeh S., Wintsky S., Lin H., Satorius C.,
 RA Vemuri R., Aletas A.H., Wen H., Epstein N.D.;
 RT "The overall pattern of cardiac contraction depends on a spatial
 gradient of myosin regulatory light chain phosphorylation."; Cell
 107:631-641(2001).
 RL [5]
 RN STRUCTURE BY NMR OF 577-602.
 RP MEDLINE=92263094; PubMed=1585175;
 RA Ikura M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Bax A.;
 RT "Solution structure of a calmodulin-target peptide complex by
 multidimensional NMR."; Science 256:632-638(1992).
 CC -!- FUNCTION: Implicated in the level of global muscle contraction and
 cardiac function (by similarity). Phosphorylates a specific serine
 in the N-terminus of a myosin light chain.
 CC -!- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
 light-chain] phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Colocalizes with phosphorylated
 myosin light chain (RLCP) at filaments of the myofibrils.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
 CC
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; J05194; AAA31400.1; -;
 DR PIR; A35021; A35021.
 DR PDB; 2BBM; 31-JAN-94.
 DR PDB; 2BBN; 31-JAN-94.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW ATP-binding; Phosphorylation; Acetylation; 3D-structure.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT DOMAIN 296 551 PROTEIN_KINASE.
 FT DOMAIN 272 279 POLY-PRO.
 FT DOMAIN 585 597 CALMODULIN-BINDING.
 FT NP_BIND 302 310 ATP (BY SIMILARITY).
 FT BINDING 325 325 ATP (BY SIMILARITY).
 FT ACT_SITE 417 417 BY SIMILARITY.
 FT CONFLICT 335 335 K -> KK (IN REF. 2 AND 3).
 FT HELIX 581 596
 FT TURN 596
 SQ SEQUENCE 607 AA; 65337 MW; 6E677641751A04C8 CRC64;
 Query Match 5.3%; Score 465.5; DB 1; Length 607;
 Best Local Similarity 29.2%; Pred. No. 9, 2e-10;
 Matches 131; Conservative 86; Mismatches 174; Indels 57; Gaps 13;
 QY 43 LHSLEPALPGPSPMQVTIEDVQAQTGTAQFAAIEGDP-----QPSVTWYKDSVQLVD 96
 DB 156 LHS-----PSCPAAIIASTEKLPAPKPLSEASELIFEGVPATPGPTPPGPAKEGGVDLLA 210
 QY 97 STRLSQOQEG-----TTSYLVRHVASKDAGVYVTCIAQNTGGQVLC---- 137
 DB 211 E---SQEAGEKAPGQADQAKVQGDTSRGIEFQAVPSE-----RPRPEVQALCLPAR 260
 QY 138 KAEILLVGGDNEPDSKQSHR-----RKLHGFYEV--KEEIGRGVGFVKVQVHKGNKI 189
 DB 261 EEDCFQILDDCPPPAPPFPHRIVELATGNVSSEFNSKEALGGKGFAGVCTCTEKSTGL 320
 QY 190 LCAAKFPPLRS--RTAAQAVREDRDLAALSHPLVTLGDDFETRKLILILELCSSEELLD 248
 DB 321 KLAAKVKKQTPKDKEMWLEEVNQLNHRNLIQLYAAIEPHEIVLFMEVIEGGLPE 380
 QY 249 RLVRKGV-VTEAEVKYVIOQLVEGLHSHGVLDHKPKSNILMVHPAREDIKICDFGF 307
 DB 381 RIVDYDYLTEVDTMVFVRQICDGLFMEKRVLHDLKPFENILCVNTTGHVLKIDFGL 440
 QY 308 AQNITPAELQFOYSGSPFVPELIQQNPVSEASDIWAMGVISYLSLTCSSPAGESDRA 367
 DB 441 ARYNPNEKLKYNFGTFPELSEVNVYDQISKTWNLSGVITYMLLSGLSPFLDDDTTE 500
 QY 368 TLNVLEGRVSWSPMAHLSEDAKDFIKATIQAPQAPRPSAAQCILSHFWFKLSPASEA 427
 DB 501 TLNNVLSGNWYFDEETFEAVSDEAKDFVSNLIVKEQGARMSSAAQCLAHWP-LNNL-ASKA 558
 QY 428 HFINTK-----QLKPLLRSRWQRSLMS 450
 DB 559 KRCNRRLKSQLLKXLMKRWKKNFIA 586
 RESULT 15
 ULK1 HUMAN STANDARD; PRT; 1050 AA.
 ID ULK1 HUMAN
 AC O75385;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase ULK1 (EC 2.7.1.-) (Unc-51-like kinase
 1).
 DE ULK1.
 GN ULK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98360094; PubMed=9693035;
 RA Kuroyanagi H., Yan J., Seki N., Yamanouchi Y., Suzuki Y.-I.,
 RA Takano T., Muramatsu M.-A., Shirasawa T.;
 RT "Human ULK1, a novel serine/threonine kinase related to UNC-51 kinase

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 23, 2004, 15:04:47 ; Search time 63 Seconds
(without alignments)
8338.695 Million cell updates/sec

Title: US-10-697-263-2
Perfect score: 8740
Sequence: 1 MGCCRLGCGCSVAHSVSG.....RNRKERRALLYKRNLAQVR 1665

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_nhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_porcine:*
- 11: sp_reptile:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvrius:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6898	78.9	1319	4 Q9HCD3	Q9hcd3 homo sapien
2	1913	21.9	2242	4 Q9P2P9	Q9p2p9 homo sapien
3	1864	21.3	3262	11 Q9EQJ5	Q9eqj5 mus musculus
4	1547.5	17.7	341	11 Q8QUP9	Q8qup9 mus musculus
5	898.5	10.3	1171	11 Q8QTF7	Q8qtf7 mus musculus
6	824	9.4	8081	5 Q7Z120	Q7z120 caenorhabdi
7	818	9.4	799	11 Q8BZF4	Q8bzf4 mus musculus
8	701.5	8.0	1393	5 Q7Z119	Q7z119 caenorhabdi
9	695.5	8.0	1226	5 Q9W1D6	Q9w1d6 drosophila
10	695.5	8.0	3197	5 Q9W1D5	Q9w1d5 drosophila
11	580.5	6.6	1042	11 Q8QW23	Q8qw23 mus musculus
12	552	6.3	1721	5 Q961U1	Q961u1 drosophila
13	552	6.3	8943	5 Q9VAF7	Q9vaf7 drosophila
14	551.5	6.3	8625	5 Q8EGD6	Q8egd6 procambarus
15	541	6.2	992	4 Q9COL5	Q9col5 homo sapien
16	541	6.2	1914	4 Q7Z4J0	Q7z4j0 homo sapien

17	538	6.2	929	5	O01651	O01651 drosophila
18	536.5	6.1	1289	4	Q9V2A5	Q9v2a5 homo sapien
19	536	6.1	641	6	Q9B3E9	Q9b3e9 macaca fasc
20	536	6.1	2959	11	Q9TIF1	Q9tifi rattus norv
21	531	6.1	6588	5	O76281	O76281 drosophila
22	529	6.1	523	5	Q8MLD7	Q8mld7 drosophila
23	529	6.1	1506	5	Q9V7G6	Q9v7g6 drosophila
24	529	6.1	4463	5	Q8MLD8	Q8mld8 drosophila
25	529	6.1	9270	5	Q8MLD9	Q8mld9 drosophila
26	528	6.0	611	11	Q91XS9	Q91xs9 cavia porce
27	526	6.0	4736	5	Q7VT99	Q7vt99 mytilus gal
28	523.5	6.0	2780	5	Q8MNS0	Q8mns0 caenorhabdi
29	523.5	6.0	2808	5	Q8MNS1	Q8mns1 caenorhabdi
30	523.5	6.0	18519	5	Q8ISF6	Q8isf6 caenorhabdi
31	519.5	5.9	1129	11	Q8OUX0	Q8oux0 mus musculu
32	508	5.8	1950	11	Q8QYX9	Q8qyx9 mus musculu
33	507	5.8	18534	5	Q8ISF7	Q8isf7 caenorhabdi
34	506.5	5.8	878	5	Q9GV22	Q9gv22 mytilus gal
35	504.5	5.8	832	5	O01653	O01653 drosophila
36	503	5.8	2693	5	Q8ISF3	Q8isf3 caenorhabdi
37	501.5	5.7	1031	11	Q8QYN7	Q8qyn7 mus musculu
38	501	5.7	907	13	Q988E0	Q988e0 carassius a
39	500	5.7	785	5	Q8MLD6	Q8mld6 drosophila
40	498	5.7	6831	5	Q23550	Q23550 caenorhabdi
41	498	5.7	7158	5	Q23551	Q23551 caenorhabdi
42	497.5	5.7	732	5	Q9GTV1	Q9gtv1 drosophila
43	496	5.7	786	5	Q9GV79	Q9gv79 drosophila
44	492	5.6	724	11	Q8BWD1	Q8bwd1 mus musculu
45	489	5.6	448	11	O54784	O54784 mus musculu

ALIGNMENTS

RESULT 1

Q9HCD3 PRELIMINARY; PRT; 1319 AA.
ID Q9HCD3
AC Q9HCD3;
DT 01-MAR-2001 (TREMSLrel. 16, Created)
DT 01-MAR-2001 (TREMSLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMSLrel. 25, Last annotation update)
DE Hypothetical protein KIAA1639 (fragment).
GN KIAA1639.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20450693; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro."
RL DNA Res. 7:273-281(2000).
DR ENBL; AB046859; BAB13465.1; -.
DR HSSP; P56276; 1TLX.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003951; FN.II.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008266; Tyr_kinase_As.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00069; pkinase; 2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00060; FN3; 1_kinase; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 KW Hypothetical protein; ATP-binding; Immunoglobulin domain; Transferase.
 FT NON-TER 1
 SQ SEQUENCE 1319 AA; 142049 MW; FBA43AE17204EF48 CRC64;
 Query Match 78.9%; Score 6898; DB 4; Length 1319;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1318; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 345 AMGVISYLSLTCSPFFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKDFIKATLORAPQ 404
 DB 1 AMGVISYLSLTCSPFFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKDFIKATLORAPQ 60
 QY 405 ARPSAAOCLSHPWFLKSWPAEAEHFNITKQLFLLARSRWQSLMSYKSLVMSRIPELL 464
 DB 61 ARPSAAOCLSHPWFLKSWPAEAEHFNITKQLFLLARSRWQSLMSYKSLVMSRIPELL 120
 QY 465 RGPDPSELGVARHLCDRTGTGSSSSSSSSONELAPFAFAKSLPPSPVTHSLHPRGFLR 524
 DB 121 RGPDPSELGVARHLCDRTGTGSSSSSSSSONELAPFAFAKSLPPSPVTHSLHPRGFLR 180
 QY 525 PSASLPEAEASERSTAP 584
 DB 181 PSASLPEAEASERSTAP 240
 QY 585 APGRRHPARRRHLLKGGYIAGALPGLREPLMEHRVLEEAAREEQATLLAKAPSPETAL 644
 DB 241 APGRRHPARRRHLLKGGYIAGALPGLREPLMEHRVLEEAAREEQATLLAKAPSPETAL 300
 QY 645 RLPSAGTHLAPCHSHSLHSDSPSTPRSSSEACGAQLPSAPSGCAPIRDMXGHPQGSQOL 704
 DB 301 RLPSAGTHLAPCHSHSLHSDSPSTPRSSSEACGAQLPSAPSGCAPIRDMXGHPQGSQOL 360
 QY 705 PSTGHPGTAQPERPSPDPGQAPFCHPKQGAPOEGCGPHPAVAPCPGPPSPGSCCK 764
 DB 361 PSTGHPGTAQPERPSPDPGQAPFCHPKQGAPOEGCGPHPAVAPCPGPPSPGSCCK 420
 QY 765 EAPLYPSFFFLGQAPAPAKASPLDCKMGPGDISLPGPKPGPCSPGSAQASQSSQ 824
 DB 421 EAPLYPSFFFLGQAPAPAKASPLDCKMGPGDISLPGPKPGPCSPGSAQASQSSQ 480
 QY 825 VSSLVGVSSGVGTERTPGSLDAEGMTQEAEDLSSTPTLQRPQEQVTKRKFSLGGRGGYAG 884
 DB 481 VSSLVGVSSGVGTERTPGSLDAEGMTQEAEDLSSTPTLQRPQEQVTKRKFSLGGRGGYAG 540
 QY 885 VAGYGTFAFGDAGWLGQPMWARIWAVSQSEEEERARASQSEEQEAEAEPLP 944
 DB 541 VAGYGTFAFGDAGWLGQPMWARIWAVSQSEEEERARASQSEEQEAEAEPLP 600
 QY 945 QVSARVPVEVGRAPTRSSPEPTPWEDIGQVSLVQIRDLSDGDAEADTISLDSISEVDPAYL 1004
 DB 601 QVSARVPVEVGRAPTRSSPEPTPWEDIGQVSLVQIRDLSDGDAEADTISLDSISEVDPAYL 660
 QY 1005 NLSLDYDIKYLPEFEMI FRKVPKSAQPEPPSPMAEELAEPEPTWMPGELGPHAGLEI 1064
 DB 661 NLSLDYDIKYLPEFEMI FRKVPKSAQPEPPSPMAEELAEPEPTWMPGELGPHAGLEI 720
 QY 1065 TESEEDVDALLAEAVGRKRWSSPSRSLFHPGRHLPLDEPAELGLRERVKASVEHISR 1124
 DB 721 TESEEDVDALLAEAVGRKRWSSPSRSLFHPGRHLPLDEPAELGLRERVKASVEHISR 780
 QY 1125 ILKGRPEGLKSGPPKPKGLASFRISGLKSWDRAPTLRELSDTIVVLGQSVTLACQVS 1184
 DB 781 ILKGRPEGLKSGPPKPKGLASFRISGLKSWDRAPTLRELSDTIVVLGQSVTLACQVS 840
 QY 1185 AQFAAATWSKQAPLLESSSRVLI SATLKNFOLLILVVAEDLGVTCSVSNALGTVT 1244
 DB 841 AQFAAATWSKQAPLLESSSRVLI SATLKNFOLLILVVAEDLGVTCSVSNALGTVT 900
 QY 1245 TGVLRKAERPSPPCPDIEGVADGVLLVWKPVESYGPVTYIVQCSLEGGSWTTLASDIF 1304
 DB 901 TGVLRKAERPSPPCPDIEGVADGVLLVWKPVESYGPVTYIVQCSLEGGSWTTLASDIF 960

QY 1305 DCCYLTSKLSRGVTVTFTACVSKAGMGPYSSPSEQVLLGPGSHLASSEESQGRSAQPLP 1364
 DB 961 DCCYLTSKLSRGVTVTFTACVSKAGMGPYSSPSEQVLLGPGSHLASSEESQGRSAQPLP 1020
 QY 1365 STKTFAFOTQORGFSSVVRQCEKASGRALAAKIIPYHPKDKTAVLREYALKGLRHPH 1424
 DB 1021 STKTFAFOTQORGFSSVVRQCEKASGRALAAKIIPYHPKDKTAVLREYALKGLRHPH 1080
 QY 1425 LAQLHAAVLSPRHLVILLELCSGPPELLPCLAEASYSSESEVKDYLMQMLSATQVYLNQHI 1484
 DB 1081 LAQLHAAVLSPRHLVILLELCSGPPELLPCLAEASYSSESEVKDYLMQMLSATQVYLNQHI 1140
 QY 1485 LHLDIRSENMITEYNLLKVVLDLGNQSLSOBKVLPSDKFKDYLETMAPELLEGGQVAPQ 1544
 DB 1141 LHLDIRSENMITEYNLLKVVLDLGNQSLSOBKVLPSDKFKDYLETMAPELLEGGQVAPQ 1198
 QY 1545 TDIIWAIGVTAFTMLSAEYFVSSEGARDLQRLKGLVRLSRCYAGLSGGAFAFURSTLCA 1604
 DB 1199 TDIIWAIGVTAFTMLSAEYFVSSEGARDLQRLKGLVRLSRCYAGLSGGAFAFURSTLCA 1258
 QY 1605 QPWGPFPCASSCLOCWLTTEGPACSRPAPVTPPTARLVEFVNRREKRALLVKRNLQAV 1664
 DB 1259 QPWGPFPCASSCLOCWLTTEGPACSRPAPVTPPTARLVEFVNRREKRALLVKRNLQAV 1318
 QY 1665 R 1665
 DB 1319 R 1319
 RESULT 2
 Q9P2P9 PRELIMINARY; PRT; 2242 AA.
 ID C9P2P9
 AC C9P2P9
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Hypothetical protein KIAA1297 (fragment).
 GN KIAA1297.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirotsawa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes.XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB037718; BAA92535.1; -.
 DR HSP; P56276; ITLK.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR00719; Prot kinase.
 DR InterPro; IPR008271; Ser_Thr_kin_AS.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; ig; 5.
 DR Pfam; PF00069; pkinase; 2.
 DR ProDom; PD000001; Prot kinase; 2.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 2.


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Db 2788 APTSGPTRAPPPDPTSLAPTALAPPASQASTLSPTSSMSANQALSSLKAVGPPPAT 2847
QY 1346 -----PSHLASEEE-----SQGRSAQPLSTKTFAP-- 1371
Db 2848 PPKRKGILLATQAAEBSPPSIVVTSEPRSFVDDTGITLPTSSPGCVKPAFSSISLYNVT 2907
QY 1372 -----OTQIQORGFVSVCQWEKA 1390
Db 2908 SFVSAPPAPAPAPPEPPPEPTKVTVRSLSPAKEVVSSTPSTTLRQGFLENPTPSWRRR 2967
QY 1391 SGRALA-----AKIIPYHPKDKTAVLREYALKGRHPLAQLAAALYSP 1435
Db 2968 PGCALACGHAGRMRAERLSPRFVPAEAGKRRVLQEVLTLLHRLSLHEAVITP 3027
QY 1436 RHLVLTLELCSGPPELLCLAEASVSEVKYLQWLSATQYLHNLQHLHLDRSENMI 1495
Db 3028 RYLVLVAESCGNRELCCGSDPRYSDDVATYVVQLLQGLDYLGRHHVHLHDIKPNLL 3087
QY 1496 ITEYNLLKVVLDGNAQSLSQEKVLPDSKFKDYLETWAPLELGGQAVPQTDIWAIGVTAF 1555
Db 3088 LAADNALKIVDFGSAQPYNPQALKPLGHRTGTLEFMAPEMVKGDPIGSAITDINGAGVLYT 3147
QY 1556 IMLSAEYVSSSGARDLQRLKGLVRLSRVAGLSGAVAFRLSTLCAQWGRPCASSC 1615
Db 3148 IMLSGYSPFYPDPQTEARIIVGGRFDAFQLYPNTSQSATFLRKVLVSHVFWSPSLQDC 3207
QY 1616 LQCPMLTERGPACSRPAPVPTFTARLRFVVRNREKRALLYKRNHL 1661
Db 3208 LAHPWLQDAYLMKLRQITLFTTNLKSFLGQRERRAEATRKV 3253

RESULT 4
ID Q80UP9 PRELIMINARY; PRT; 341 AA.
AC Q80UP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LOC216790 protein (Fragment).
GN LOC216790.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleth P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
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RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046431; AAH46431.1; -.
DR GO; GO:0005524; F.ATP binding; IEA.
DR GO; GO:0004674; F.protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F.protein-tyrosine kinase activity; IEA.
DR GO; GO:0004868; F.protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT NON_TER 1
SQ SEQUENCE 341 AA; 38078 MW; 63BDB2E3FFD71914 CRC64;

Query Match 17.7%; Score 1547.5; DB 11; Length 341;
Best Local Similarity 87.7%; Pred. No. 1.2e-91;
Matches 299; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

QY 1326 VSKAGNGPYSPSEOVLLGGPSHLASEE-SQGRSAQPLSTKTFATQIQORGFVSVR 1384
Db 1 VSKAGNGPYSPSEOVLLGGPNHLASEEESRGRPAQLLPSTKTFATQIQORGFVSVR 60

QY 1385 QWKEASGRALAAKTIIPYHPKDKTAVLREYALKGRHPLAQLAAALYSPRHLVLI 1444
Db 61 QCREKASGRALAAKIVPQPEDKTAVLEYEALKELHPLAQLAAALYSPRHLVLI 120

QY 1445 CSGPELLCLAEASVSEVKYLQWLSATQYLHNLQHLHLDRSENMIITYNLLKV 1504
Db 121 CSGPELLCLAEASVSEVKYLQWLSATQYLHNLQHLHLDRSENMMVTEYNLLKV 180

QY 1505 VDLGNAQSLSQEKVLPDSKFKDYLETWAPLELGGQAVPQTDIWAIGVTAFIMLSAEY 1564
Db 181 IDLQNAQSLDQEKVPAPENFKDYLETWAPLELGGQAVPQTDIWAIGVTAFIMLSGEY 240

QY 1565 SSEGARDLQRLKGLVRLSRVAGLSGAVAFRLSTLCAQWGRPCASSCLOCQPWTEE 1624
Db 241 SSEGTRDQLKRLKGLIRLSRCYAGLSGAVAFQSSLCQWGRPCASTCLOCQWTEE 300

QY 1625 GPACSRPAPVPTFTARLRFVVRNREKRALLYKRNHLAQVR 1665
Db 301 GPTGSRPTPTFTVRLRAFAVREHREKRALLYKRNHLAQVR 341

RESULT 5
ID Q80TF7 PRELIMINARY; PRT; 1171 AA.
AC Q80TF7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MKIAA1297 protein (Fragment).
GN MKIAA1297.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
RL EMBL; AK122488; BAC65770.1; -.
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DR GO: GO:0005524; F-ATP binding; IEA.
 DR GO: GO:004674; F-protein serine/threonine kinase activity; IEA.
 DR GO: GO:004713; F-protein-tyrosine kinase activity; IEA.
 DR GO: GO:004648; P-protein amino acid phosphorylation; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN III-like.
 DR InterPro: IPR003599; IG-like.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG-C2.
 DR InterPro: IPR00719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00041; fn3.1.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Prot_kinase.1.
 DR SMART: SM00409; IG.1.
 DR SMART: SM00408; IG2.1.
 DR SMART: SM00220; S_TK.1.
 DR SMART: SM00219; TYRK.1.
 DR PROSITE: PS00835; IG LIKE.1.
 DR PROSITE: PS00111; PROTEIN KINASE DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 FT NON_TER
 SQ SEQUENCE 1171 AA; BAE413056089AE57 CRC64;
 Query Match 10.3%; Score 898.5; DB 11; Length 1171;
 Best Local Similarity 24.5%; Pred. No. 5.6e-49;
 Matches 318; Conservative 130; Mismatches 468; Indels 381; Gaps 29;
 QY 611 LREPLMEHVRLEBAAREQATLLAKAPSETAURLPASGTHLAPGHSLEHDS-----665
 DB 1 LRGPL-----LESGLR-----ARDPRMARASSEAAHPHQPSPESRGLQKSSFSQ 48
 QY 666 PSTPRPSSEACAEQRLSPAGGAPIRDMGHPQ-SKQLPSTGGHPG-----TAQPE-717
 DB 49 EAEPGRHRRAGAPLEIPVALGARRLQESLSALSSETQPPSPARFVPKLSTTKSP 108
 QY 718 -----RPSDPSWGQAPFCHPKQGSAPQECSP--HPAVAPCPFGSPFGSCKEAPLVP 770
 DB 109 SAVTSDSPQPEQVPEKVPKPEPVRAAKPAQALQMPQLTPVAIQMSLQL 168
 QY 771 SPFFLQQAQAPAPAKASPPDLSDXMGPGDISLPGPKPGPCSSGASQSSQVSLRV 830
 DB 169 SPPTL-SFQDP-----AVPSEPKHAAVFAVVASPPGV-----SEKRVPSARTPPVLA 217
 QY 831 GSSQVGT---PFGPSLDAEGTQEAEDLSDSTPLTPQEQVMTKFSLGGRGYAGVAG 887
 DB 218 EKARVPTVPPRFGSSLSGSIENLESEAVFEA--FKRSRESPLSGRL-----264
 QY 888 YGTFAGDAGGMLQGPWARIWAVSQSEEEQEEARABESQSEEEQEEARABESPLQVS 947
 DB 265 -----LSRSEERGGPFGAEDDGIYRSPAGTPL-----294
 QY 948 ARPVEVGRAPTRSPPEPTMEDIGQVSLVQIRLSGDAEAADTISLDISEVDPAYLNL 1007
 DB 295 -----ELVRPERGERS-----VQDLVAGEPGLVRLSLSLQK-----328
 QY 1008 DLYDKYLFPEFMFRKVPKSAQPEPPSPMAEBELAEFPPTWPGELGFHAGLEITEE 1067
 DB 329 -----LRRTPPQGR-----HPAMESRSGDG-----ES 350
 QY 1068 SEDVDALLAAVAGKRWKSSPSRLFH-----FGRHLPLDEPAELGLRER 1114
 DB 351 SEGSSARASPVAVRRLLSTLERLSRLORSOSSSDSGASGRSTPL-----FGLRR 405
 QY 1115 VKASVEHISRI-----LKGRRPEGLKBP-----R 1140
 DB 406 ATSEGESLRLRGVPHNOLGSGTATTPSABSLGSEASGTSAPGESRRHRWGLSLR 465
 QY 1141 KKPGLASRLSGL-----KSWDRAPTLRLSDETVGLQSVTLACQVSAQPA 1189
 DB 466 KXGLSQNLSSVQEDLGHQVPSDSDFPVFHIKQVLLGEAATLLCLLPACAP 525

QY 1190 QATWSDKAPLESSRVLISATLKNFOLLITLVVAEDLGVTCTSVNALGTVTTGVLR 1249
 DB 526 RISWMDKQSLRSEPSVWIVSCDKGQLLIPAGKRHAGLYECSATNLVLSITSCVTA 585
 QY 1250 XAERPSSPCPDIGEVYADVGLVWLPVSEYSGVTVIVQCSLEGGS-WTTLASDIFCCY 1308
 DB 586 VARIPGKLAPPEVPQYHTALTALVWKPGRAPCTYTLERRVDGESVWHFVSSGIDCY 645
 QY 1309 LTSKLSRGGTYTERTACVSKAGMGPISSPSEQVLLGG-----1345
 DB 646 NVQLPVGTVTRFVACSNRAGGPPSPSEKVFIRGTPDSPAQAAPAPDAPVTSGPTR 705
 QY 1346 -----PSHLA-----1350
 DB 706 APPDPSLAPTPALAPPASQASTLSPSTSSMANQALSSLKAVGPPATPPKRHGLL 765
 QY 1351 -----SEES-----QG-----1357
 DB 766 ATQQAEPSPSIVVTPSEPSFVPDGTGILTPISSPGQVAPAPSSLYVWTFVSPAPAP 825
 QY 1358 -----RSAQPL-----PSTKTFAPQTOIGRSPSVVR 1384
 DB 826 QAPAPPPPEPTKVTVRSLSPAKEVSSPTSTTLRQGPQPKPYTFLEKARGRGVVR 885
 QY 1385 QCVKASGRALAAKIIPYHPKDKTAVLREYALKGLRHPHLAQLHAAVLSPRHLVILEL 1444
 DB 886 SCRENAIGTFAKIVFYAAGKRRVQLQYEVLRILHRLMSLHEAYITPRYLVLIAES 945
 QY 1445 CGPELLPCLAPRASYSSEVDYLMQMSLATCYLHQHILHLDRSENMIITEYNLLKV 1504
 DB 946 CGNRELLCGLSDRFYSDDVATVYVQLQGLDYLHGHVHLHDIKPDNLLAADNALKI 1005
 QY 1505 VDLGNAOSLSQEKVLPSEKFDKYLETMAPELLEGGQVAPQTDIWAIGVTAFTMLSAEYV 1564
 DB 1006 VDFGSAQPNQALPKLGHRTGTLEFMAPEWVKGDPISGATDINGAGVTVIMLSGYSF 1065
 QY 1565 SSEGARDLQGRKGLVRLSRVYAGLSGGAFLRSTLCAQWGRPCASSCQCPLWTEE 1624
 DB 1066 YEPDQETEARIVGGFADFQLYPNTSQSATFLKVLVSHVHWSRPSLQDCLAHFWLQDA 1125
 QY 1625 GPACSRPAPVPTTARLVRVFNREKRALLYKRNIL 1661
 DB 1126 YLMKURQTLTFTTNRLKEFRGEQRRRAEAATRHKV 1162
 RESULT 6
 Q72120 PRELIMINARY; PRT; 8081 AA.
 AC Q72120; 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Uncoordinated protein 89, isoform b.
 GN UNC-89.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RL investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Du Z., Le T.T., Wilson R.;
 RT "The sequence of C. elegans cosmid C09D1.";
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

773	QY	PFLGOPOAPPAPAKAS-----PPDLSKM--GPGDISLP-GRP--KPQGPCSSPFGSA	817
7215	Db	-----QPGELLIPAKVYSDSLAGLPAADKKVLEDAENDPSPVGAFLFLEGLHGSDLTI	7270
818	QY	SOASSQVSLRVGSSQVGTBPGLSDAEGWTQEAEDLSDSTPTTLQRPQOVMTMRKFSLG	877
7271	Db	DTTSASGL--IKVTSFPAINLSPNK-----SPRSTPTGKSPVVLSPRQSHMEVLIAT	7322
878	QY	GRGGYAGVAGYGTFAFGDAGMLCQGPWARIANAWSQSESEEBEAEAEASQSEBQEEA	937
7323	Db	KGK-----KPGFLPZGEL-----AEDIDDEDAFMDDRKKQ----	7352
938	QY	RABSLPOVSARPVPEVGRAPTRSSPEPTPWEDIGQVSLVQTRDLSDAEAD-----	990
7353	Db	-----TISL-DISEVDPA--YLNLSDL-----YDIKYLPEE--FMI---FRKVPKSAQPE	1032
991	QY	-----DKNRIVNLDDLCKYRPAFYKDDSDGFHGPGYDIDATPMDSHYQIGPDYTLMAARGA	7433
1033	QY	PPSPMAEBELABFPPTFWPPELG-PRHAGLBIITESEVDALLABAAVGRKKKSNPSPR	1091
7434	Db	SRVRYRBELEFGMGAPTVK-QQFLGVRNRDITVRERRRYTD-ILRETTQGLEPKSHEQST	7491
1092	QY	SLFHPFGRHLPLDEBAPAEGLRERVKASVSHI8KILLGRDEGLEKEGPPRKKPGLAGFRLS	1151
7492	Db	AL-----LQAPSATAIBRIKADIKVTPC-----ATKNDGDTF---7526	7526
1152	QY	GLKSWDRAPTFURELSDEFVLVGGQVTLACQVSAQPAQAATWSKQCAPLESSRVLISAT	1211
7527	Db	-----APIFTARLDVYLRKNQPAIFCAVSASPAKVTWDFQOKILESNDRVVTIEQD	7579
1212	QY	LKNFOLLTLVVVAEDLGVYTCVSNALGTVTATTGVLKRAERPSSPCPDIGEVAD-GV	1270
7580	Db	NNVAELILNHAAPDYDLGEVCTAINEYXTDKSSCRLISGETPSRPGRPE-AELSSDTEI	7637
1271	QY	LIVWKPVESYGP-----VVIYVQCSL-----EGSWTTLASDIFDCYLTLKSLRGTYT	1320
7638	Db	FIQWEAPE--GPTYLEGITYRLEYRVAGENDHGDPMITVSEKIDBSVIVKHLSPGLIYQ	7695
1321	QY	PRTACVSKAGMGYP-----SPSEQV-----LLCGPSH	1348
7696	Db	FVTAQNGFGLGLPSLSSRIVQTHGKGA PKLQIDVLKSEIRLNVMSMPKSTNQLGISE	7755
1349	QY	LASEBESQGRSA-----QPLSTKTFAPQIQGRGSVVVQCWEKAS-GRALA	1396
7756	Db	-ESEDSEARTANEDKMSNLQJTDPTGRQFQIGGLKGRFSFVIANDVSTTEGHACHCA	7814
1397	QY	AKIIPVHPKDTAVLREYBALKGLRHPHLAQLHAAVLSPRHLVILELCSGPELLPLCAE	1456
7815	Db	VKI--RHPSE--AISEYBSLDGQHENVQRILIAFNNSNFLYLLSERLY-EDVFSRFV	7869
1457	QY	RASYSESEKOVLMQMLSATQVILHNOHIIHLDRSENMIITEYN--LLKVVVDLGNQSL	1514
7870	Db	NDYYTEQVALTMRQVTSALHFLHFGIAHLDVNPNHINPQSKRWSVKLVDFGRQAKVS	7929
1515	QY	QEKVLPSDKFYDLET--MAPEL-LEBQGAVPQTDIWAIGVTAFIMLSAEYPVSSSEGARD	1571
7930	Db	-GAVKEVD-----FDIKWASPEPHIPETPTVQSDNMWGMGVVTFCLLAGEPHPTSE--YD	7981
1572	QY	LQGLRKLGLVLSRCYAGL-----SGGAVAFRLSTLCAQPGWGPCASSCQCQWLTBEGP	1626
7982	Db	RESEIKENWINV-KCDPNLIPVNASOECLSFATWALKSPVRRTDEALSHKFLSSDPS	8040
1627	QY	ACSRPAPVTFPTARLR	1642
8041	Db	MVRRRSIKYSASRLR	8056

RESULT 7

Q8BZF4

ID

Q8BZF4

AC

Q8BZF4

PRELIMINARY;

PRT;

799 AA.

PRELIMINARY: PRT: 799 AA.

DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical tyrosine protein kinase/serine/threonine protein
DE kinase/eukaryotic protein kinase/fibronectin type III domain
DE containing protein (Fragment).
GN APEGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RC MEDLINE=22354683; PubMed=12466851;
RA the PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RL ENBL; AK035543; BAC29098.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:109282; Apegl.
DR GO; GO:0005824; F1ATP binding; IEA.
DR GO; GO:0004674; F1protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F1protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P1protein amino acid phosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG-C2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; ED000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein.
FT NON_TER
FT SEQUENCE 799 AA; 86397 MW; A15C45E37FBA14A2 CRC64;
Query Match 9.4%; Score 818; DB 11; Length 799;
Best Local Similarity 29.4%; Pred. No. 5e-44;
Matches 205; Conservative 83; Mismatches 234; Indels 176; Gaps 7;
QY 1140 RKXPGLASFLSLG-----KSWDRAFTFLRELSDETIVLGQSVTLACQVSAQPA 1188
DB 93 RKDKGLSQNLSSVQEDLGHQVPSSEDFPFVFIKLDQVLLGEAATLLCLPAACPA 152
QY 1189 ACATWSKDGAPLESSRSRLISATLKNFQLTLVWVAEDLGVYTCVSNALGVTTTGV 1248
DB 153 PRISWMKQSLRSESVIVSVCKDGRQLSLPRAGKRHAGLYECSATNVLSITSCV 212
QY 1249 RKAERSSPCPDIGEVADGVLLVWKPVESGPTVIYVQCSLEGS-WTTLASDIEDCC 1307
DB 213 AVARIFGKLAPEVPQTYHTALVWVKPGDGRAPCTYTLERRVDGESVWHPVSSGIPDCY 272
QY 1308 YLTLSLRGCTYFTRTACYSKAGMGFPYSPSPQVLLGG----- 1345
DB 273 YNVTQLPVGVTVFRVACSNRAGOGFPSPSEKVFIRGTPTDSPAQAAAPRDPVTSPT 332
QY 1346 -----PSHLA----- 1350

DB 333 RAPPDPSPTSLAPTALAPPASQASTLSFSTSSMSANQALSSKAVGPPPPPPKRRHGL 392
QY 1351 -----SEES-----QG----- 1357
DB 393 LATQAEPSPPSIVVTPSEPRSPVDPDTGTLTFTSPQGVKAPSPSTSLYMTSVFVSAPPA 452
QY 1358 -----RSAQPL-----PSTKTFAPQTQIQGRFSV 1383
DB 453 PQAPAPPEPPEPTKVTVRSLSLPAKEVSSPTPSTTLRQGPFPKPYTFLEEKARGFGV 512
QY 1384 RCWEKASGRALAAKIIIPYHPKDKTAVLRVEALKRHLRHPHQAOLHAAYLSPRHLVLILE 1443
DB 513 RSCRENATGRTEFAKIVPAAGKRVLOEVEVTLTHERELMSLHEAYITPRVLVIAE 572
QY 1444 LCGPELLPCLAEPRASYSESEVKYLMQMLSATYLNQHLHLDLSENMITEYNLLK 1503
DB 573 SCGNRELLCGSLDRFYSSEDDVATVVLQGLDYLGHVHLHLDIKPDNLLLAADNALK 632
QY 1504 VVDLGNAGLSLSEKVLPSDKFVDLETMAPELLEGQGAVPOTDIWAGVTAFAIMLSAEP 1563
DB 633 IVDFGSAQPNPQALKPLGHTGTLEFVAPENWVGDPISGATDIWAGVLTIMLSGYS 692
QY 1564 VSSEGARDLORGLRGLVRLSRVAGLSGGVAFLRSTLCAPWGRPCASSCLOCPLWTE 1623
DB 693 FYEPDPPQTEARIVGGREFDAFQLYPNTSQSATLFLRKVLVHPWSPRSLODCLAHPLQD 752
QY 1624 EGPACSRPAPVPTPTARLVRVNRKERRALLYKRHL 1661
DB 753 AYLMKLRQTLTFTTNRLKEFLGERRRRAEAATRHKV 790
RESULT 8
Q72119
ID Q72119 PRELIMINARY; PRT; 1393 AA.
AC Q72119;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Uncoordinated protein 89, isoform C.
GN UNC-89.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodexinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z., Le T.T., Wilson R.;
RT "The sequence of C. elegans cosmid c09D1.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003131; AAP68959.1; -.
SQ SEQUENCE 1393 AA; 156296 MW; F947C1BCE4EB9CE9 CRC64;
Query Match 8.0%; Score 701.5; DB 5; Length 1393;
Best Local Similarity 22.3%; Pred. No. 3.7e-36;

	Matches	364;	Conservative	212;	Mismatches	580;	Indels	475;	Gaps	639
QY	211	DILAALSHPLVLTDLQGFETRKLII	LELCSSEELDLRYKGVVTEAEVKYIIQOLVE	270						
Db	14	DGLSSLAHPGV	-----ETAE-----	PKGVNRET	CVRVFVRQLLI	47				
QY	271	GLHYLSHGVLHLDIKESNITLMVH	PAREDIKICDPGPAQNITPAELQFSQYSGSEPFVSPE	330						
Db	48	ALGHMEDLRFAHDLRLPETILL---	QDDKUKLADFGQARRLLRGLTGEIKSGSEPFVSPE	104						
QY	331	IIQONFVSEASDIWAGVIVSYLTS	CSPPAGESDRATLLNVLEGRVSWSSPMAAHLSED	390						
Db	105	IVRSYPLTLATDMWSTGVLTIV	LTGLSPFHGDNDNETLANVDSQCFD--SSPL--GNFSYD	162						
QY	391	AKDFIATLQORACQARPSAAC	QIUSHPWF---LKSMPAEAEHATINTKQLKFLARSRWQR	446						
Db	163	AGDFVKLLTEIEIVSRLLTV	DEALDHPMINDEKLTPE-----LSADTLREFKYQHKKWLE	216						
QY	447	SLMSYKSILVMRS---	IPELLRGP-----PSPSLGVARHLCR-----	481						
Db	217	-----RRVFOQTPSEQLLEA	ILGPATAQQAQNPVAPEGERRPAEIVDYILRIQPKKPPT	271						
QY	482	-----DTGGSSSSSSSDNE---	LAPFARAKSLPPSP-----VTHS---	514						
Db	272	VEYVQPRKEHPFIDFGQLIDG	ADPRDEGTGFEGRHPQPPIQPPQRPNQAAHDSR	331						
QY	515	-----PLHPRGLRPSASL	PERAEASERSTEAPAPASPEGA	552						
Db	332	RHEQQPHQOQOPRIPVDYGR	PLVDPR--YLNDPSHRPSSLDADPTVYKGVNPHVDKY	390						
QY	553	GPAAACQCPRHVSIRSLFYHQA	GESPEHGALAPGSRHRHPRARRHLKGGYIAGALPG--	610						
Db	391	GRPWA-----PQNLK	RKLIQDCKGETSHS--KKEKTCHPVATPIL-----	ASPQGD	436					
QY	611	-----LRPLMEHRVLEBEAR---	EEQATLLAKAPSPETALRLPASGTHLAPGH	657						
Db	437	QQQOKIPMRMIRGERREIEE	IANRILDISEGSIAGSLASLED--FEIP-----	K	486					
QY	658	SHSLEHDSPTPRPSSACGEA	QRLSAPSGGAPIRDMGHPOGSKQLPGTGGHPGTAQPE	717						
Db	487	DFQVEASEPTPLTPE-----	VTIRE-----TIPKP	513						
QY	718	RPSPDPSWGQAPFCHPKQ	GSAPQEGCSPHAVAPCFPGSPGCSKEAEPLVPSSPFLGQ	777						
Db	514	TPSPTSPOKSPVP-----	-----	Q	527					
QY	778	QAPPPAKAS-----PPLDS	KM---GPGDISLP--GRP--KPGPCSSPGSASQSS	822						
Db	528	PQGLLIIPAKVYSDSIAGU	PAADKKVLEDAENDPSIPVGAPLEGLHGSDLTIDTISA	587						
QY	823	SQVSSLRVSGSVQGTGEP	SLDAEGMTQEABDLSDTPTLQRPQEVMTMRKFSJGGRGY	882						
Db	588	SGL--IKVTS	PAINLSPK-----SPRSTPGTKSPVVLSPRQEHSMEVLIATKRG--	637						
QY	883	AGVAGYGTFAFGGAGG	MLGQGFPMWARIAMVSSQEEQEEARAEASQSEEQEAREASP	942						
Db	638	-----KPGFLPPGEL---	-----AEDIDDDAFNDORKKQ-----	664						
QY	943	LPQVSARPVPEVGRAPTR	SSPEPTWEDIGQVSLVQIRDLSDGDAEAD-----	990						
Db	665	-----	-----VKPKDHGDENDXKERLEKDKNVR	690						
QY	991	TISL-DISEVDPA--YLNLS	DL-----YDIKYLPEF--FMI-----FRKVPSKAQPEPSPM	1037						
Db	691	TVNLDLDDKYRPSAFYKDD	SDFGHPGYDIDATPWDSHYQIGPDYILMAARGAATNSVRVN	750						
QY	1038	AEELAEFPPEPTWPGBELG-	PHAGLETTESBDVALLAAAVGRKKWBSPPSRSLPHF	1096						
Db	751	YREELFGMAFTVK--QGF	LVNRNDITVRRRRYTD--ILRETTQGLEPKSHEQSTAL---	805						
QY	1097	PGRHLPLDEPAELGLR	ERVKASVEHISILKGRPEGLEKGGPRKPGCLAGFRUSGLKSW	1156						
Db	806	-----LOKAPSATAIER	IKADIEKVTPC-----ATKNDNDGTG-----	838						

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RESULT 9
Q9WID6
ID ID Q9WID6 PRELIMINARY; PRT; 1226 AA.
AC Q9WID6; Q961J6;
DT 01-MAY-2000 (T-REMBUREl. 13, Created)
DT 01-OCT-2002 (T-REMBUREl. 22, Last sequence update)
DT 01-OCT-2003 (T-REMBUREl. 25, Last annotation update)
DT DT 01-OCT-2003 (T-REMBUREl. 25, Last annotation update)
DE DE Q930171 protein (GH20492p).
GN B8ST:HL01080 OR CG3901 OR CG18019 OR CG18020 OR CG18021 OR CG30101.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_taxid=7227;
RX [1]
RX SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RC MEDLINE=20136106; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RX Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RX George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RX Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RX Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,
RX Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RX Allred J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RX Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RX Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RX Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RX Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RX de Pablos E., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimios I., Simpson M.C., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskae R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.-
 RA Zeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*,"
 RT Science 287:2185-2195(2000).
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DR	GO; GO:0005524; F1ATP binding; IEA.	
DR	GO; GO:0004674; F1protein serine/threonine kinase activity; IEA.	
DR	GO; GO:0004713; F1protein-tyrosine kinase activity; IEA.	
DR	GO; GO:0016740; F1transferase activity; IEA.	
DR	GO; GO:0006468; F1protein amino acid phosphorylation; IEA.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR008987; FN_III-like.	
DR	InterPro; IPR003599; IG.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR000719; Prot_kinase.	
DR	InterPro; IPR002290; Ser_thr_kinase.	
DR	InterPro; IPR001245; Tyr_kinase.	
DR	Pfam; PF00041; fn3; 1.	
DR	Pfam; PF00069; kinase; 2.	
DR	ProDom; PD000001; Prot_kinase; 2.	
DR	SMART; SM00060; FN3; 1.	
DR	SMART; SM00409; IG; 2.	
DR	SMART; SM00219; TyrKc; 1.	
DR	PROSITE; PS00835; IG_Like; 1.	
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 2.	
DR	ATP-binding; Transferase.	
KW	SEQUENCE 1226 AA; 142191 MW; 7892F7B352D3D307D5 CRC64;	
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	Best Local Similarity	18.5%; Pred No. 7,5e-36;
	Matches 305; Conservative 209; Mismatches 513; Indels 625; Gaps 41;	
QY	63	VQQTGTHQTFPAITEGDPQPSVTYKDSVLVSTRLS-CQEGTYSVLVSHVASKA 121
DB	86	IMARKG--RIEAKLVGIPLPVHFVFKDWKIPVSSRIKISSYDDPIVLSHIDSIKGG 143
QY	122	GVTYTLAQNQTGGVLCABELLVGLGDNFDPSEKSHRR-----KLHSFYEVKEEIG 172
DB	144	GLYSISARNIAGSI--STSVTHIENEDQVIYKTYGRHPVRSKQLRYQDKYDIGELG 201
QY	173	RGVGFQVVRQVHGKNIILCAKFIPLRSRTAQAYRERDILALSHPLVTGLLDQFETRK 232
DB	202	RTGQGTYYHAYVRSSGDNVAAIKYGRLELPFMLEWNTFNHKNLRIPYDAVDTDR 261
QY	233	TLILILELCSBELL--DLRYRGVVYTEAEVKYVQQVLEGLYHLHSHGVLLHDKFESNII 291
DB	262	SVTILMELAAAGSELVRDNLRRDYTERDIAHYRQTGLWLEHHMGVGHMGLTIKDLL 321
QY	292	MVHPAREDTIKCDFPAQNIIPAEIQFQSQSPSFVPEIIQQNPVSEASDIWAMGVISY 351
DB	322	ISVVGDIKVSDFGLSKRINKHNLSLDYGNPFVSVFVNKEGVNFSDHMTVGLIITY 381
QY	352	LSUTCSSPAGSSDRATLNLVLEGRVSSSPMAHLSADAKDFIKATLQAPQAPSAQA 411
DB	382	VLGGHNPLGIDDRETTLTKREGSDWPKDINWTHISDDGRDFISRLLLYSPEERMDVKT 441
QY	412	CLSHPWFLKSPAEAAHFINTKQLFLARGRWQSLMSYKSLVWRSIPELLRGPPDSP 471
DB	442	ALKEPHF-----FMLDRPVYDHY-----460
QY	472	SLGVAR-----HLCDTGGSSSSSSSDNLELAFARAKSLPPSPVTHSLPHRGLRP 525
DB	461	QIGTDLRNLNYDHF-RDWYANASCKN-----YFRREL-----492
QY	526	SASLPEAEASERSTEAPAPSPAGAPPAQCQCPRHVSIRSLFYHQAGSEPHGALA 595
DB	493	-----SCGF-----496
QY	586	PGSRHRPARRHLLKGGYIAGNALPGLREPLMEHVRVLEEAAREQATLLAKAPSFETALR 645
DB	497	-----QPSKMY-----504
QY	646	LPASGTHLAPGHSHLSHDSFSTRPSEACGEAQRLPSPAGAPIRDWGHPQGSQQLP 705
DB	505	-----PEGHVYTFE-----NTEPLPEPRIRAKR-----EEVV 532

RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RP
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AE003442; AAF47134.2;
 DR FlyBase; FBgn0040499; BEST:HUG1080.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004674; P:transferase activity; IEA.
 DR GO; GO:0006458; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003599; Ig_III.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00047; ig; 15.
 DR Pfam; PF00069; Pkinase; 2.
 DR Prodom; PD000001; Prot_kinase; 2.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00409; IG; 21.
 DR SMART; SM00408; IGG2; 18.
 DR SMART; SM00220; S_TKG; 2.
 DR SMART; SM00219; Ty_KG; 1.
 DR PROSITE; PSS0835; IG_LIKE; 14.
 DR PROSITE; PSS0011; PROTEIN KINASE DOM; 2.
 DR ATP-binding; Immunoglobulin domain; Transferase.
 SQ SEQUENCE 3197 AA; 361286 MW; F43E74689B455A3B6 CRC64;

Query Match	8.0%	Score	695.5	DB	5	Length	3197		
Best Local Similarity	18.5%	Pred. No.	3.1e-35						
Matches	305	Conservative	209	Mismatches	513	Indels	625	Gaps	41
QY	63	VOATGTTAOFEAII	EGDPPSVVTKDSVQLVDS	TRLSS-QQOEGTTVSLVLRHVASKDA	121				
DBb	2057	IMARKNG-RIEAKLVGIP	PLPVEVHFQDKWPIDVDSRIKISSYDPDVIYLSIHDSIKDG	2114					
QY	122	GVYTCLAQNTGGQVL	CKRELLVJGGDNEDPSKQSHRR-----KLMSFEVFEKEIG	172					
DBb	2115	GLYE:SARNIAGSI--	-STSVTHIEENEDQYTKTYGRHPYVRSKQLRYQDKYDIDGELG	2172					
QY	173	RGVGFVKRVQHKGNKIT	CAAKFIPURSTRACQAYRERDILAAASHPLVLTGLLDQETRK	232					
DBb	2173	RGTCQITVHAVERSSG	NDVAAKIWYGRPELRFFMLNELEMNTFNHKNLRPYDAYVDTOR	2232					
QY	233	TLIILILCISRELL--	DRLYRKQVTEAEVKYIQCLVEGLHYLHSHGVHLQIKSNIL	291					
DBb	2233	SVTILMELAGGELVRLN	LRDDYYTERDIAHYIQTLLWGLEHHVGVGHMGLTKDLL	2292					
QY	292	MVHPAREDIKIDFGFAQ	NITPAELOFCYQSGPEFVSPETIQQNPVSEASDIWAMGVISY	351					
DBb	2293	ISVVGGDIIKVSDFGL	SRKINRHNLTLDYGMPFVSPVNVNKGVNFSDMMTVGLITY	2352					
QY	352	LSLTCSSFPAGESDRAT	LINVLGKRVSWSSPAAHLSEDAQDFKATIQAPQAPSAQ	411					
DBb	2353	VLLGGHNPFGIDRE	DTLTKIRGWRDWFKDEITWTHISDDGRDFTSRLLLYSPERMDVKT	2412					
QY	412	CLSHPWFLKGMPAEEA	HAHFINTKQLFKLLARSEQWRLSKYSKILVMRSIIPELLRGPPDP	471					

Qy	1497	TEYNLL--KVVDLGNQAQLSQ--EKVLPSDKFYDYLETMAPELLBSGQAVPOTDIWAIGV	1552
Dd	3006	ASVRGIQKLVDFSGAKVKNLGMKWVTCGS---LDFOPEMINDEPIFQSDIWSLGA	3061
Qy	1553	TAFIMLSAEYPVSSSEGLDLQRGLRKLVLRSRYAGLSGGAVAFIRSLTLCAQPWGRFPCA	1612
Dd	3062	LTLYLLSGCSPPFGADEYETKQNIISFVRYVFENLFKEVTPEATRTFMILLFKRHPTKSPYT	3121
Qy	1613	SSCLOCPWLTEEGPACSPAPVTPETARLNVF	1644
Dd	3122	ECLCHRWLMSSDYWRKERAIPLGSLKTF	3153
 RESULT 11 Q80W23 PRELIMINARY; PRT; 1042 AA.			
ID	Q80W23		
AC	Q80W23;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DE	01-OCT-2003 (TrEMBLrel. 25, last sequence update)		
DE	01-OCT-2003 (TrEMBLrel. 25, last annotation update)		
DR	trio protein (fragment).		
GN	TRIO.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxID=10090;			
[1]	SEQUENCE FROM N.A.		
RP	TISSUE=olfactory epithelium;		
RC	MEDLINE=22386257; PubMed=12477932;		
RX	Strausberg R.I., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.P., Caavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Willalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettawan M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences".		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
[2]	SEQUENCE FROM N.A.		
RP	TISSUE=olfactory epithelium;		
RC	Strausberg R.;		
RL	Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC051169; AAH51169.1; -		
DR	GO; GO:0005524; P:ATP binding; IEA.		
DR	GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	InterPro; IPR001849; PH.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR000219; RhoGEF.		
DR	InterPro; IPR003290; Ser_thr_kinase.		
DR	InterPro; IPR008271; Ser_thr_pkin_AS.		
DR	InterPro; IPR001452; SH3.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	Pfam; PF00047; Ig_1.		
DR	Pfam; PF00169; PH_1.		

DR	GO; GO:0005524; F-ATP binding; IEA.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO; GO:0016740; F:transferase activity; IEA.
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR	InterPro; IPR003962; FNIII subd.
DR	InterPro; IPR003961; FN III.
DR	InterPro; IPR008957; FN-III-like.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003598; IG_c2.
DR	InterPro; IPR006162; Pfantne_S.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	InterPro; IPR008271; Ser_thr_pkin_AS.
DR	Pfam; PF00041; fn3; 3.
DR	Pfam; PF00047; ig; 8.
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DR	ProDom; PD000001; Prot_kinase; 1.
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DR	SMART; SM00408; IGC2; 5.
DR	SMART; SM00220; S_TKC; 1.
DR	PROSITE; PS50835; IG LIKE; 8.
DR	PROSITE; PS00012; PHOSPHOPANTHEINE; 1.
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW	ATP-binding; Immunoglobulin domain; Repeat; Transferase.
SQ	SEQUENCE 1721 AA; 193936 MW; 500774BIIE81EFB93 CRC64;

Query Match	6.3%;	Score 552;	DB 5;	Length 1721;
Best Local Similarity	18.6%;	Pred. No. 2.3e+26;		
Matches	313;	Conservative 172;	Mismatches 453;	Gaps 51;

QY	48	PALPGPPSMQVTTEDVOAQGTGAPEAIEGDPQSVTWYKDSVLVDSTRLSQQOEGT	107
DB	430	PQAASPLIVKPLRDANCIONHNAQTCTTINGVPKPTISWYKGAREISNGARYHMYSEG	489
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QY	108	TYSILVRHVASKDAGVYTCLTAQNTGVOLCKALLV	143
DB	490	NHFLINDVFGEADAEYVCRAVKAGAKSTRATLAIMTAPKANVPRFRDTAYFDKGENV	549
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QY	144	-----	143
DB	550	VIKIPFGFPKPRIHWVRDGENTESGGHYTVVEKERHAVLIIRDGSHLDGSPRYRTAENE	609
	:	:	:
QY	144	LGPD-----NEPS-----EKQSH---	157
DB	610	LGSDTAIQVQISDRPDPFRLIESIGTSLSWKAPWDGSDITNYYVERREHLPS	659
	:	:	:
QY	158	-----	157
DB	670	SWIRVGNTRFTSMAVSGLTGKEYDFRIPADNVYGRSDASDTSLTIKTESVKKPKTER	729
	:	:	:
QY	158	-----RRKLHSFEYKEISIGGVFG	177
DB	730	WEIDANGKRKLKGADGPVKDYDSYVFDIYSKFVEQPVEISQQSYVDYDILESIGTAGFG	789
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QY	178	FVKEVQHGNKILCAAFIPL-RSRTRAQYRRERDILAALSHPLVTGLLLDQCFTRKTLIL	236
DB	790	VVHCRESRSTGNIIFAAKFI PVSHSVEKDILRREDINNQLHHQKLIHLHADFDDDEML	849
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QY	237	ILELCSEELLDRLYRGK-VVTEAEVKVIQQLVEGLHYLHSHGVHLHDIKPSNILMVHP	295
DB	850	ILEFLSGELPERITAEGYVMTEAEVNYMRQCICEGRHMHBQNIIHLDIKPENIMCQTR	909
	:	:	:
QY	296	AREDIKICDFGAQNIPTAELOFSQYGSPFVSPEIIQQNPVSEASDIWANGVISYLSLT	355
DB	910	SSTNVKILDFGLATRLDNEVVKITGTAEPAARFEIVNREFPVGYTDMATGVLSYLLS	969
	:	:	:
QY	356	CSSPFAGESDRATLLNLLEGVSNSSPVAHLSEDADFKATIQAPAPAPSNAQCLSH	415
DB	970	GLSPFAGNDVQTLKNVACDWDFVESFYKISEAKDFIKLLVRNKERTMAHECLLH	1029

Db	1701	AVSGKA 1706	
AC	Q9V4F7	PRELIMINARY; PRT; 8943 AA.	
DE	CG32013-PA.		
GN	BT OR CG32019.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,		
RA	Abriel J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,		
RA	Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cauley S.A., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,		
RA	Jalali M., Kaluher F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,		
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D., Scheier F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,		
RA	Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,		
RA	Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,		
PT	"The genome sequence of Drosophila melanogaster."		
RL	Science 287:2185-2195(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,		
RA	Hradecky P., Huang Y., Kamnik J.S., Prochuk S.E., Smith C.D.,		
RA	Tu J.L., Bergman C.M., Berman B.P., Carlson J.W., Celisner S.E.,		
RA	Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,		
RA	Harris N.L., Kronmiller B., Marshall B., Milburn G.H., Richter J.,		
RA	Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,		
RA	Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,		
RA	Lewis S.E.,		
PT	"Annotation of Drosophila melanogaster genome."		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	FlyBase;		
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RA	FlyBase;		
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB003843; AA59316.4; -		
DR	FlyBase; EBN0005666; bc.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR000577; FGK kin.		
DR	InterPro; IPR003962; FNIIT subd.		
DR	InterPro; IPR003961; FN III-like.		
DR	InterPro; IPR008957; FN III-like.		
DR	InterPro; IPR003959; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003598; IG C2.		
DR	InterPro; IPR006162; Pplantn S.		
DR	InterPro; IPR000719; Prot kinase.		
DR	InterPro; IPR002290; Ser Thr kinase.		
DR	InterPro; IPR008271; Ser Thr_kin_AS.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	Pfam; PF00041; fn3; 39.		
DR	Pfam; PF00047; ig; 26.		
DR	Pfam; PF00069; pkinase; 1.		
DR	PRINTS; PR00014; FNTYPEIII.		
DR	ProDom; PD000001; Prot kinase; 1.		
DR	SMART; SM00060; FN3; 40.		
DR	SMART; SM00409; IG; 38.		
DR	SMART; SM00408; IG2; 29.		
DR	SMART; SM00220; S_TKC; 1.		
DR	SMART; SM00219; TYRK; 1.		
DR	PROSITE; PS00933; FGK KINASES 1; 1.		
DR	PROSITE; PS00835; IG LIKE; 30.		
DR	PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.		
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.		
DR	PROSITE; PS00011; PROTEIN KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN KINASE_SI; 1.		
SQ	SEQUENCE 8943 AA; 1001276 MW; 786EA35A4E62ED47 CRC64;		
Query Match	6.3%; Score 552; DB 5; Length 8943;		
Best Local Similarity	18.6%; Pred. No. 2,6e-25;		
Matches	313; Conservative 172; Mismatches 453; Gaps 51;		
Qy	48 PALPGPPSMQVTTEDVQAQTGGTAQFAIEGDPQPSVTWYKDSVLVDSTLSQQCEGT 107		
Db	7652 PQAAAPPLIVKPLRDANCIONHNAQFTCTINGVPKFTISWYKGAKEISNGARYHMYSEG 7711		
Qy	108 TYSILVLRHVASKDAGVYVTCIAQNTGGVCLCKAELLV----- 143		
Db	7712 NHFLINDVFGEDAEYVCRVAVNKAAGAKSTRATLAINTAPKLVPPRFRDTAYFOKGENV 7771		
Qy	144 ----- 143		
Db	7772 VIKIPFTGPKPIHVRGNIENSGHYTVVKERHVAVLIRDSGLDSDGPRYRTAENE 7831		
Qy	144 LGGD-----NEPDS-----EKQSH----- 157		
Db	7832 LGSDTALIQVSDRDPDRPPLIESIGTESLSLWKPWPGCSDTNYYVERREHPLS 7891		
Qy	158 ----- 157		
Db	7892 SWRVGNTRFETSMVSGLPFGKEYDPRFADNVYGRSDASTSLTKESVKKPIERK 7951		
Qy	158 -----RRKLHSFYEVKEEIGRGVFG 177		
Db	7952 WEIDANGKRLGRKADGVKDYVDFYISKVPQVPEISQSVYDVIDLEILGTFGAF 8011		
Qy	178 FVKRVQHKGNKILCAAKFTPL-RSRTRAQAYERDILALSHPLVTGLDQDQETKTLIL 236		

8012	VVHRCRSTGNVFAAKFIPVSHSVSEKOLIRREIDIMNOLHQKLINLHDAFEDDEMI	8071
237	IILECSSBELLDRYRKXG-VVTEAEYKVYIQQLVEGLHYLHSHGVHLHDIKPSNIMVHP	295
8072	IIEFLSGGELFERITAEYGVYMTAEVINYARQICEGIRHMEBQNIHLHDIKPENIMCQR	8131
296	AZEDKICDFGAQNIITPAELQSQVSGSEFVSPEITIQONVSEASDIWANGVSYLSLT	355
8132	STNVKLLDGLATRLDPNEVVKITGTGTAEFAPELVNREPVGFTYDWATGVLSYVLLS	8191
356	CSSPAGBSDRATLLNVLEGRVWSSPMAAHJSEDAKFIKATLQAPQAPSPAAOCLSH	415
8192	GLSPFAGDNVDYITUKNVKACDWDPDFVESFKYISEAKDFIRKLLVRNEKEMTAHECLH	8251
416	PWFLKSPMAEBAHINTKQLKFLLASRMORSIMSYKSLV-----MRSEPELLGPP	468
8252	PWLTGDHSAKQE-INRD--RYLAYREKLRYKEZEFERFLPIGRLSYSSIRKLL-----	8304
469	DPSLUGVARIHCRDTGSSSSSSSSSNEELAPFAKAKSLPPSVTHSLPHRPGFLRPSAS	528
8305	-----MSKYIHD-----AVFDRQAA-----PRFVIRPS--	8329
529	LPEEAESERSTEAPAPPASPAGPAAQCQVPRHSVIRSLFYHOAGESPEHGALAPGS	598
8330	-----SQCVEGQSV--KFYCR-----	8345
589	RHPARRHLKGYIAGALPGTREPDMHRVLEBEAREEOATLAKAPSE-----	641
8346	-----IAIATPTL--TWSHNNIE-----LRQSVFKRYVGD	8376
642	-----TALRLPASGTHLAPGSHSLSHDS-----PSTPRSPSEACGEAQLRPSAPSGAPI	692
8377	YVFIINRVKLDORGEYIIRAEHVGSREEVFLVQPLPKEQ-----PYRTESTPV	8428
693	RMGHGPQSKOLPSTGHPDTAQPERSPDPSWGPQAPFCHPKQGSAPQECSPHAPAP	752
8429	R-----RRBFLPYTFW-----QE-----	8441
753	CPGSPFPGSCKEAPLVSPFFLQQAAPPAPAKASPLDSKWPGD-----ISLPGRPX	807
8442	-----ESETAPSTFLLRPV-----MQARDCKLLCLLSGKPV	8475
808	BPCSSPGSAQSSSQVSLRVGSSQVGTGPGPSLDAEGWTQAEADLSDBSTPLQEPQE	867
8476	P-----NVR-----WKGRELSUYEVANTHSDG	8499
868	QVTMRKFLSGRGYAGVAGYGTAFG DAGMLGQGPWARIAWVSQSEEEQBARA	927
8500	VVTMB-----	8504
928	ESQSEEQEAREASPLQVSNRPVPEVGRAPTRSSPEPTMEDIGOVSLVQIRLSDAE	987
8505	-----IIOCKP-----SDSGKYS--KATNCHGTDE	8528
988	AADTISLSDIVDPAYLNLSD--LY--DIKYLFFBMFRKVPKSAQPEPSPMAEBELA	1043
8529	TDCVIVVEGVTWTEQAQLAHNLYSGDRKY-----EQIPKAPLPIVTSR	8575
1044	BPEEPTWPCGELGPHLAGLITSESDVDALLA--EAAVGRKRWKSSPSRSLFHPGHR	1100
8576	QVTS-----SSVQNTSEPGQDKVNSVNSNGISNKKYIANS--LQAPG--	8618
1101	LPLDEPAELGLRVERKVASBHSIRILKRGPELKEGPPRKKPGLAGLSPRSLGKSWDRAP	1160
8619	-----SPSRSRSATKELLIPDDDSLMCKP	8642
1161	TFRLSPDETIVVLGQSVTLACQVSAQAPAAQTWSXDGAPLBSSSSRVLISATLKN--POLLT	1219
8643	ETKPELHDLTTHDGEQILITCYKGDPPEQIWSNRNGKSLSSD--ILDLRYKNGIATLTT	8700
1220	ILVVAEDLGVYTCVSNALGVTTTGVL-----RKAERPSSP-----	1258
8701	INEVPPEDEGVITCTATNSGVATETCKLTIOPLDKNINKRWAGDNAPKIVSHLESRF	8760

Qy	1259		-----CPDIGRVDAGVLLW-----KVESYGVPTIIVQCSLEGGSWTTLAS	1301
Dd	8761	VRGDGAVNLACRIIGAQHPD----	VVLHNNKEIKPSKDF-----OYTNEANIYRLQIA	8810
Qy	1302	DIFDCYLTSKLSRGGTYT-----FRTACVSKAGMGPFSS-----PSEQVLL	1343	
Dd	8811	EIFF-----EDGTTYCEAFNDIGESFSCTINVTVPGETKQPSFKVFPTSVSILE	8862	
Qy	1344	GPPSHLASEEESQ-----GRSAQLPST-KTFAPQTQIQGRPSV-----VRQCWEK	1389	
Dd	8863	GGGTTFECIDSELNLWLWKGFIDEITLPFRSYFTKGHRYSFAVKCNMDDVGQYQAK	8922	
Qy	1390	A-SGRA	1394	
Dd	8923	AVSGKA	8928	

RESULT 14				
Q86GD6	PRELIMINARY;	PRT; 8625 AA.		
ID	Q86GD6,			
AC	01-JUN-2003 ('REMBLrel. 24, Created)			
DT	01-JUN-2003 ('REMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 ('REMBLrel. 25, Last annotation update)			
DE	Projectin.			
DE	PROJ.			
GN	Procamburus clarkii (Red swamp crayfish).			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Plecocyemata; Astacidea;			
OC	Astacidea; Cambaridae; Procamburus.			
NCBI_taxid=6728;				
RN	[1]			
SEQUENCE FROM N.A.				
TISSUE=Muscle;				
OShino T., Shimamura J., Fukuzawa A., Maruyama K., Kimura S.;				
RA "The entire cDNA sequences of projectin isoforms of crayfish claw				
RT closer and flexor muscles and their localization.";				
RL J. Muscle Res. Cell. Motil. 0.0-0(2003).				
EMBL; AB055927; BAC66140.1; --				
GO; GO:0005743; Cmitochondrial inner membrane; IEA.				
GO; GO:0005524; F:AIP binding; IEA.				
GO; GO:0003488; F:binding; IEA.				
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.				
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.				
GO; GO:0003743; F:translation initiation factor activity; IEA.				
GO; GO:0005468; P:translational acid phosphorylation; IEA.				
GO; GO:0006413; P:translational initiation; IEA.				
GO; GO:0006810; P:transport; IEA.				
InterPro; IPR003962; FNIII subd.				
InterPro; IPR003961; FN.III.				
InterPro; IPR008957; FN.III-like.				
InterPro; IPR003599; IG.				
InterPro; IPR007110; IG-like.				
InterPro; IPR003598; IG.C2.				
InterPro; IPR003596; IG.V.				
InterPro; IPR001993; Mitoch carrier.				
InterPro; IPR000719; Prot.kinase.				
InterPro; IPR002390; Sex_thr_kinase.				
InterPro; IPR008271; Ser_thr_pkin_AS.				
InterPro; IPR001950; TIF_SUII.				
Pfam; PF00041; fn3; 39.				
Pfam; PF00047; ig; 13.				
Pfam; PF00069; pkinase; 1.				
PRINTS; PR001014; FNTYPEI11.				
ProDom; PD000001; Prot.Kinase; 1.				
SMART; SM00060; FN3; 39.				
SMART; SM00409; IG; 36.				
SMART; SM00408; IGC2; 24.				
SMART; SM00406; IGV; 3.				
SMART; SM00220; S.TKC; 1.				
SMART; SM00219; TyrcK; 1.				

RESULT 14

DR PROSITE; PS00835; IG LIKE; 24.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS01118; SU1.1; 1.
SQ SEQUENCE 8625 AA; 962637 MW; 5688B4C4FE0AFC90 CRC64;

Query Match 6.3%; Score 551.5; DB 5; Length 8625;
Best Local Similarity 18.8%; Pred. No. 2.6e-25;
Matches 291; Conservative 173; Mismatches 460; Indels 623; Gaps 43;

QY 48 PALGPPSMQVITIEDVOAGTGTGAFAEITBGPDPQPSVWTKDSVQLVDSTRLSQOQEGT 107
DB 7338 PNAATPEIITPLRNVVALQHRSAITLCQTAGKRPNIISWFKGNRELCSAKYAMNRDGD 7397
QY 108 TSVLVRHVASKDAVGYTCLANTGGQVLCCKAELLV----- 143
DB 7398 TYTLTVHVDYGEDEYMCRAQNGGIRSTRKADISIKLAPKINVPFRDRTAFFDKGENA 7457
QY 144 ----- 143
DB 7458 VIKPIFIGNPRITWOREGETIESGGHYSVETQORHAILHLRVTLDTGNVRLTAENE 7517
QY 144 LGGD-----NEPD----- 151
DB 7518 LGSDSVIKICISDRPDPRPKVESILGTECVLTWQIFLWDGGANINNVIIKRELPM 7577
QY 152 ----- 151
DB 7578 SWIRCSNTRLTATQIKGLSPGHKQFRVYAENVYGRSDPSAVTSVETPAPLTKKPKKKV 7637
QY 152 -----SEKQSHRK-----LHSFYEVKEEIGRGVFGF 178
DB 7638 YEVDTGKIKGRKESVDYDQFVFDVYKVPQVDIKHDSVYEVYDLEIEIGTGAGV 7697
QY 179 VKRVQHKGNKILCAAKFIPLRSRTAQAYR-ERDILAALSHPLVTGLIDOPETKRLTILI 237
DB 7698 VHCRCERTGNIFAAKFIPVASAMEKELIRKIDIMNHLHPKLIINLHDAFEDDDENVLI 7757
QY 238 LELCSBELLRLKRG-VVTEAEVKVYIQQLVGLHSHGVHLHDIKPSNIMLVHPA 296
DB 7758 FEFUGGSELFERITAEGVYGEAEVINYRQICGVGMHEKNIHLVDKRENIMCOTKT 7817
QY 297 REDIKICDFGAQNIITPAELOFSQYSGSPFVSPIIQONPVSEASDIWAMGVISYLSLTC 356
DB 7818 STNVKLIDFGLATKLDPNVVKISGTAEFAAPEIVEREPVGVFTDMKAVGLAYVLLSG 7877
QY 357 SSPFAGESDRATLLNVLSGRVSWSPMAHLSEDAKDFIKATLQAPQAPSAQCCLSHP 416
DB 7878 LSPFAGENDIDTLKNVXACDWDDEEAFNSVNEAKDFIRLLINKKEKMTAHECLMHA 7937
QY 417 W-----FLKSNPAEEAHFINTKQ-LKFLARSWQSLMSYKSLVMSRIPE 462
DB 7938 WLRGDSYRPLEIDMRYPIPIRDKIRAKYKAWAKFLLPGR-----LAEYSSL----- 7985
QY 463 LLRGPPDSFSLGVARHLCDRTGGSSSSSSSDNELAPFARAKSLPPSPVTHSPLLRHGF 522
DB 7986 -----RKHLDKYRIHDT-----HFDRCQA-----PRFV 8010
QY 523 LRPSASLPEEAEEA-----SERSTEAPAPPSPESGAGPAAQGC--VPRHS----- 565
DB 8011 IIPQNAFTYEGSVFSCRIVAAPFTVCFWNNMELQSVKVMKRYSGEDYSFVINRVK 8070
QY 566 -----VIRSLFYHQAGESPHEGALAPGSRHRHPARR--RHLLKGGYTAGALPGLRPLM 616
DB 8071 LEDRGYIIRAEVHYGAREEPVFLNVQPLPEAPPYRPEQIIR-----RRQPL- 8119
QY 617 EHRVLEENAREEQATLLAKAPSEETARLPLASGTHLAPGHSLSHSDSPSTPRPSSEAC 676
DB 8120 TYKLWQEEG-----EGASFTFL-----RPRVQC 8145
QY 677 GEAQLRPSAGCAPTRDMGHPQGSQKLP-----STGGHFGTAQPERPSPDFWQAPFC 732

DB 8146 HQTCKLLCC-LAGKEVPVTKVYKSGQELSKFDYSQSHADGVVTIIVN-----C 8193
QY 733 HPKQG-----SAPEGSGPHAVAPCPGPGFPPOGSCKEALVPSPLGQAPAPAK 786
DB 8194 KPADSGKYRCVATNSLGTDETSVCVIVEDRRYIETIKDL-----PPTTFAI 8241
QY 787 ASPPLDKRMGPDISLPGRPKPGPCSPGASQASSQVSSSLRVGSSQVGTBP-GPSLDA 845
DB 8242 RVDDTSSSS-----YFTTHKDGSRSTTKVEAASSSTSSAAAGAKETLKYKQDS 8296
QY 846 EGMTOEAEDLSSTPLQRPQVTRKFSGLGRGYAGVAGYGTAFAGDAGMLGQGP 905
DB 8297 TGTSTSR-----SATKELELPDD-----SLMGPPFGSG----- 8326
QY 906 MWARTAWVSQSEEBEQAESAESQEQBARAESPLPOVSARPVPEV--GRAPTRSP 963
DB 8327 -----ELPKTLAIKDGALCLKIVKGDP 8350
QY 964 EPTPWEDICQVSLVQIRDLSDGAADTISLDSISVDPAYLNLSDLYDIKYLFFEMIFR 1023
DB 8351 EP-----QVSWFK-----DGEPLSSSDIIDLKY----- 8373
QY 1024 KVPKSAQPPPPPMABEELAEFPTWPNPGLPHAGI-----EITEESDVEDALLAE 1077
DB 8374 -----RQGLASLTINEVFFEDGLVYCKAT 8398
QY 1078 AAVGRKRKWSPSRSLFHPGRHLPLDEPAELGLRERVKASVEHISRLKGRPEGLEKEG 1137
DB 8399 SSLG-----SAETCKKLSISPMEQQINGK----- 8422
QY 1138 PPRKPEGLASFLSLGLKSWDRAPTFLRELSDTIVLQSVTLACQVSAQAPAAQATWSKDG 1197
DB 8423 -----SG--RGDKLPRIQHLLSQVDPDGTHTLSCKTGATKEDVVMWLNH 8467
QY 1198 APLESSRVLISATLKNFOLLTLVVAEDLGVYCSVSNALG-----TVTITGVL--RKA 1251
DB 8468 KEIKPSKDFLY-VTEGDTYLLKIAEVFPDAGATYTCFAENDVGETFTCTLTIVIIPEGK 8526
QY 1252 ERPSPPCPDIDGVY-----ADGVLLW-----KPVSTGP 1282
DB 8527 KQPAFKKFRSQTVMGKSAFVSFKDKPLKVSWKDKGKPYDESSP 8573

RESULT 15
Q9COL5 PRELIMINARY; PRT; 992 AA.
AC Q9COL5;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Myosin light chain kinase.
GN MLCK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi A., Murata-Hori M., Hosoya H.;
RT "Hela myosin light chain kinase."
Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB037663; BAB21504.1; -
DR HSP; P56276; ITLK
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003962; F:III subd.
DR InterPro; IPR003961; F:III.
DR InterPro; IPR008957; F:III-like.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; IG2; 2.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS0835; IG LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Repeat;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 992 AA; 110185 MW; 3ABD72460983269 CRC64;

Query Match 6.2%; Score 541; DB 4; Length 992;
Best Local Similarity 24.4%; Pred. No. 5.1e-26;
Matches 140; Conservative 91; Mismatches 196; Indels 146; Gaps 7;

QY 45 SSLPALPG-----PPSQVTIEDVQAOTGGTAQPEAIIEGDPPQ 83
DB 286 SSLPVLGTSDATVKKKPAKTPPKAMPPIQFPEDQKVRAGESVELFGVGTQPI 345
QY 84 SVTVKDSVOLVDSTRLSQQEGTYSILVRHVASKDAGVYTCLAQNTGGVLCKAELLV 143
DB 346 TCTWVKFRKQIQAESHEMKVENSENGSKLTLAARQEHCGCYTLLENKLGSRQAQYNLT 405
QY 144 LG----- 145
DB 406 VDKPPAGTPCAGDIRSSLTLSWGSYDGGSAVQSIEIWDSSANKTWKELATCRST 465
QY 146 -----GDNEP-----DSEKO--- 155
DB 466 SFNVQDLLPDHEYKFRVRAINVTSEPSQSELTTVGEKPEEPKDEVEVSDDEKEPEV 525
QY 156 -----SHRKLHSFYEVEKEEIGRGVGFYKRVQHKGNKILCAAKFPLRSRTAQAYR 208
DB 526 DVRTVTINTEQKVSDFDIIEERLGSKGFGVFLVEKKTRKWAGKFKAYSAKEKENIR 585
QY 209 -ERDILAALSHPLVTGLDQFETRTLLILLECSSELLDLRYKGV-VTEAEVKYIQ 266
DB 586 QEISIMNCLHHPKLQVCYDAFEKANIWMVLEIVSGGELFERIIDEFELTERECIKYMR 645
QY 267 OLVEGLHYLHSHGVLEHLDIKPSNIMLVHPAREDIKICDFGPAQNITPAELQFSQYGSPEF 326
DB 646 QISEGVEYTHKQGIYVHLDLKPEINVCNKTGTRIKLIDFGLARLENAGSLKVLFGTPEF 705
QY 327 VSPETIQNPVSEASDIWAMGVISYLSLTCSPPAGESDRATLLNVLEGRVSNSSPMAAH 386
DB 706 VAPEVINVEPIGATDMNSIGVICVLVSLSPFMGNDNETLANVTSATWDFDEAFDE 765
QY 387 LSEDAKDTKATLQAPQAPSAACLSHPWFLKSMPEAAHFINTKQKELLARSRWQR 446
DB 766 ISDDAKDFLSNLLKMDKNNLDCTOCLQHPWLMKDTKQWEAKKLSKDKMKYMARRWQK 825
QY 447 SLMSYKSLVMSRIPEL-----LRGPPDSP 471
DB 826 TGNVRAIGRLSSMAMISGLSGRKSSTGSP 858

Search completed: April 23, 2004, 15:11:16
Job time : 99 secs